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Query Match 52.0%;
Best Local Similarity 74.2%;
Matches 1634; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rurals 2403 bp mRNA linear P.crispum mRNA for phenylalanine ammonia-lyase 3. x81159
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1 (bases 1 to 2403)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (22-AUG-1994) C. Appert, Institut fuer pflanzenwissenschaften, Eidgenoessische Technische Hochschule, Zuerich, Universitaetsstrasse 2, 8092 Zurich, SWITZERLAND Location/Qualifiers
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89. .2245
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89. .2245
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                                                                                                 1083 ACGTTAAGGCTGCTCAAAAGCTACATGAAATGGATCCATTACAAAAACCAAAACAAGACA 1142
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                                                                                                                                                  ACCTCAAGGCGGCGCAAAAGGTCCACGAAATGGACCCGTTACAGAAACCAAAACAAGATC 1151
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GATATGCTCTTAGAACATCTCCTCAATGGCTTGGTCCTCAAATTGAAGTTATCAGATCAT 1202
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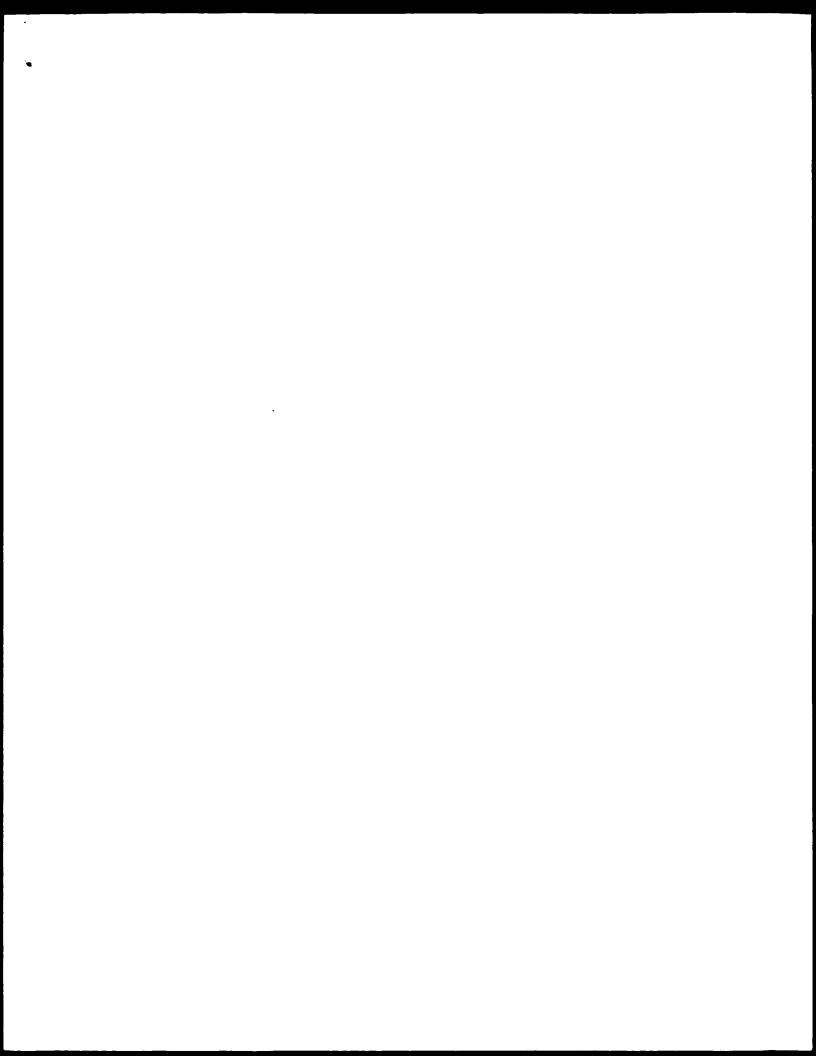
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2292 TATTCTGTTTTTTTTTTTTTTTTAAATTTTATTTGCATTT 2333
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                                                                                                                                   TGAGTATCTTACAGGAGAAAAAGTGGGGTCACCTGGGGAAAAAGTTCGAAAAAGGTATTCA
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                                                                                                                                                                                                                                                                              ACAGGATTAAAGCTTGCA5ATCGTAGCGGTTGTATAGAGTTGTAAAGGAGAGAGAGAGCTCGGCA 2111
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                                     GTGCTCCTCTCCAATCTGCTAAATTGGCATGCAGTCCAGCAATGTALTAGGAACTGTTT
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Pred. No. is the number of results predicted by chance to have a

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ALIGNMENTS

REFERENCE	ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	AF299330	RESULT 1
<pre>Bukaryota; Viridiplantae: Streptophyta: Embryophyta: Trachcophyta: Spermatophyta: Magnoliophyta: endirotyledons: core endicots: Asteridae, enasterids II, Asterales, Asteraceae, Lactuceae: Lactuca. 1 (bases 1 to 2442) Campos-Vargas, R., Nonogaki, H., Suslow, T. and Saltycit, M.</pre>	Lactuca sativa	Lactuca sativa.		AF29933U.1 GI:18001006	AF299330	Lactuca sativa phenylalanine ammonia-lyase mRNA, complete eds.	AF299330 2442 bp mRNA linear PLN 31-DEC-2001		

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hes 2442;
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                                                                                                                     TAGTTATGGTGTCACCACCGGCTTCGGCGCCACCTCTCACCGGAGAACTAAGCAAGGCGG
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                                           TGCTTTACAGAAGGAGCTCATTAGATTTTTGAACGCCGGAATATTCGGCAATGGAACGGA 540
                                                                                                                                                                                          GAGGGCTGGAGTTAAGGCCAGTAGTGATTGGGTTATGGAGAGCATGAATAAAGGAACTGA
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TGCTTTACAGAAGGAGCTCATTAGAATTTTTGAACGCCGGAATATTCGGCCAATGGAACGGA
                                                                                              TAGTTATGGTGTCACCACCGGCTTCGGCGCGCCACCTCTCACCGGAGAACTAAGCAAGGCGG
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TYLVALCQSIDLRHLEENMKSTVKNTYSQVAKKYLTMGVNGELHPSNFCEKDLLRVVD
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MDPLQKFKQDRYALRTSPQWLGPQIEVIKSSTKMIEREINSVNUNPLIDVSRNKALHG
GNEQGTPIGVSMDNTRLAIAAIGKLMEAQESELVNDEVNNGLPSNLSGGRNPSLDYGF
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RKPVVKLGGETLTVSQVAGIAAANDSDTVKVELSEAARAGVKASSDWVMESMNKGTDS
YGVTTGFGATSHRRTKQGGALQKELIRFLNAGIFGNGTETSHTLPHSATRAAMIVRIN
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/protein_id-"AAL55242.1"
/db_xref-"GI:18001007"
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100.0%; Pred. No. 0;
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Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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                                                                                381 GTAGTGATTGGGTTATGGAGAGAGATGAATAAAGAACTGATAGTTATGGTGACACCACCG 440
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                                                                                                                                                                 GT-AT-94T-AACAT955T6AA6T56A6ATTACTAATCGAAACATSCTSCGAACATSCTSCGAACATSCTSCGAACATSCTSCGAACATSCTSCGAACATSCTSCGAACATSCTSCGAACATSCTSCGAACATSCTSCGAACATSCTSCGAACATSCTSCGAACATSCTSCGAACATSCTSCGAACATSCTSCGAACATSCTSCGAACATSCTSCGAACATSCTSCGAACATSCTSCGAACATSCTSCGAACATSCTSCGAACATSCTSCGAACATSCTSCGAACATSCTSCGAACATSCTSCGAACATSCTSCGAACATSCTSCGAACATSCTSCGAACATSCTSCGAACATSCTSCGAACATSCTSCGAACATSCTSCGAACATSCTSCGAACATSCTSCGAACATSCTSCGAACATSCTSCGAACATSCTSCGAACATSCTSCGAACATSCTSCGAACATSCTSCGAACATSCTSCGAACATSCTSCGAACATSCTSCGAACATSCTSCGAACATSCTSCGAACATSCTSCGAACATSCTSCGAACATSCTSCGAACATSCTSCGAACATSCTSCGAACATSCTSCGAACATSCTSCGAACATSCTSCGAACATSCTSCGAACATSCTSCGAACATSCTSCGAACATSCTSCGAACATSCTSCGAACATSCTSCGAACATSCTSCGAACATSCTSCGAACATSCTSCGAACATSCTSCGAACATSCTSCGAACATSCTSCGAACATSCTSCGAACATSCTSCGAACATSCTSCGAACATSCTSCGAACATSCTSCGAACATSCTSCGAACATSCTSCGAACATSCTSCGAACATSCTSCGAACATSCTSCGAACATSCTSCGAACATSCTSCGAACATSCTSCGAACATSCTSCGAACATSCTSCGAACATSCTSCGAACATSCTSCGAACATSCTSCGAACATSCTSCGAACATSCTSCAACATSCTSCAACATSCTSCAACATSCTSCAACATSCTSCAACATSCTSCAACATSCTSCAACATSCTSCAACATSCTSCAACATSCTSCAACATSCTSCAACATSCTSCAACATSCTSCAACATSCTSCAACATSCTSCAACATSCTSCAACATSCTSCAACATSCTSCAACATSCTSCAACATSCTSCAACATSCTSCAACATSCTSCAACATSCTSCAACATSCTSCAACATSCTSCAACATSCTSCAACATSCTSCAACATSCTSCAACATSCTSCAACATSCTSCAACATSCTSCAACATSCTSCAACATSCTSCAACATSCTSCAACATSCTSCAACATSCTSCAACATSCTSCAACATSCTSCAACATSCTSCAACATSCTSCAACATSCTSCAACATSCTSCAACATSCTSCAACATSCTSCAACATSCTSCAACATSCTSCAACATSCTSCAACATSCTSCAACATSCTSCAACATSCTSCAACATSCTSCAACATSCAACATSCTSCAACATSCTSCAACATSCTSCAACATSCTSCAACATSCTSCAACATSCTSCAACATSCTSCAACATSCTSCAACATSCTSCAACATSCTSCAACATSCTSCAACATSCTSCAACATSCAACATSCAACATSCTSCAACATSCTSCAACATSCAACATSCTTSCAACATSCAACATSCAACATSCAACATSCAACATSCAACATSCAACATSCAACATSCAACATSCAACATSCAACATSCAACATSCAACATSCAACATSCAACATSCAACATSCAACATSCAACATSCAACATSCAACATSCAACATSCAACATSCAACATSCAACATSCAACATSCAACATSCAACATSCAACATSCAACATSCAACATSCAACATSCAACATSCAACATSCAACATSCAACATSCAACATSCAACATSCAACATSCAACATSCAACATSCAACATSCAACATSCAACATSCAACATSCAACATSCAACATSCAACATSCAACATSCAACATSCAACATSCAACATSCAACATSCAACATSCAACATSCAACATSCAACATSCAACATSCAACAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Evidence for multiple copies of formate dehydrogenase genes in plants: isolation of three potato fdh genes, fdhi, fdh2, and fdh3 (Arcession Nos 249492, Z94494) and AlEn4829, respectively). (PGR98-102)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 (bases 1 to 2322)
Mazeyrat,F.A.
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2 (bases 1 to 2322)
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Similarity 81.1%;
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/gene-"PAL"
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GNEQGTP1GVSBDNTRLAIAALGKVTIAQFSELVNDEYNNGLSHSILSGGRNPSLDSGF
KGGEIAMASY,SELGELANEYI INIVESAEUHNDVNSLGLISARKTAEXDAILKLIKSS
TYLVACTQS154PHLEENMESTVKNTVSQVAFKVLTMGVVTELHIFSBFGEKDLLRVVD
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/protein_id-"CAA/3065.1"
/db_xref-"GI:2887304"
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AVGPAGEVLNAESAFAQAGVEGGFFELQPKEGIALVNGTAVGSGMASMVLFEANVLAL
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/translation="MENGTHYNGSANGFCIKDPLNWGVAAFALTGSHIPFYKKMYGEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start-1
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0; Mismatches 420;
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                                                                     ACGGGTTCAAAGGTGGAGAAATCGCCATGGCTTCTTACTGTTCTGAGCTTCAGTTTCTCG
                                                                                                                                                                                  ATTTCTACAACAATGGATTACCATCGAATCTCTCCGGTGGACGTAACCCTAGTTTGGACT 146C
                                                                                                                                                                                                                                                                                                                                                                        GTCTCGCCATTGCTGCAATCGGAAAACTCATGTTCGCTCAATTTTCTGAGCTGGTTAACG 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAGCTTTACACGGTGGTAACTTCCAAGGAACCCCAATCGGAGTTTCCATGGACAACACCC
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AUTHORS

Yun,S.J.,

Lee, B.K.,

Park, M.R.,

Srinivas, B.

and Chun, J.-C

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VERSION
KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          114 TAATAATGGAGAACGGTAATCACGTTAATGGAGTCGTTAATGAGTTGTGCATCAAGGATC 173
                                                                                                                                                                                                                                                                                                   GAACTGATTAGGTGTCACCACCGGCTTCGGCGCGCCACCTCTCACCGGAGAACTAAGC 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TATCAATGGAGAATGGGGCACCACCACCTCGAACGGGTTGTGCGTGGAGACTACGCGTGATC 168
AAGGTGGTTGCTTCAGAAGGAGCTCATTAGGTTCTTTGAATGCCGGAATATTTCGGCAACG 522
                                                                                                                                                              AAGGCGGTGCTTTACAGAAGGAACTCATTAGATTTTTGAACGCCGGAATATTCGGCCAATG 533
                                                                                                                                                                                                                                    GGACTGACAGTTATGGAGTTACAACGGGTTTTGGTGGCACGTCACATAGGAGGACTAAAC 462
                                                                                                                                                                                                                                                                                                                                                                      AGACTERCGCGTGCGGGGTTAAGGCCGAGTAGCCATTGGGTTATGGAGAGTATGAATAAAG 402
                                                                                                                                                                                                                                                                                                                                                                                                         CGCAGGTGGCGGCGATCGCGGCGAGGGGA-----TAATGCGGTTGGCGGTTGGAGCTTGGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTCAGGTGGCGGGATCGCAGCTGCTAATGACAGTGACACCGTGAAGGTGGAGCTGTCGG 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGATGGTGGAGGAGTTCAGGAAGCCGGCGGTGAAGCTCGGCGGTGAGAGCCTGACTATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGATGGTTGCGGAGTTCAGAAAGCCGGTGGTGAAGCTCGGAGGAGAGAGGCGCTTACAGTTT 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGTTGAACTGGGTGGGGGGGGGGGAGATCGTTGAAGGGGAGCCACCTGGACGAGGTGAAGA 228
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Submitted (23-JHL-2001) Faculty of Biological Resources Sciences,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chonbuk National University, 664–14 Tokjin-donq, Chonju, Chonbuk 561–756, Republic of Korea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rhemannia glutinosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Molecular characterization of phenylalanine ammonia lyase gene in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             h 52.7%;
Similarity 72.6%;
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EIAMASYCSELQFLANPVTNHVQSAEQHNQDVNSLGLISSRKTVEALDILKLMSSTYL
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VTSV FAEVMNGKPEFTDHLTHKLKHHPGQLEAAATMEHTLDGSAYVKAAQKLHETDP
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RRPAVKLGGESLTIAQVAAIAARDNAVAVELAETARAGVKASSDWYMESHNKGTDSYG
VTTGFGATSHRRTKGGGALQKELIRFLNAGIFGNGTESHALPBISATRAAMLVRAUTL
LGGYSGIRFEILFALTKFLNHNITPCLPLRGTITASGDLVPLSYIAGILTGRPNSKAV
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/protein_id-"AAK84225.1"
/db_xref="GI:15100059"
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114. .
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/cultivar-"Keumsan"
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/EC_number-"4.3.1.5"
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                            1240 CACCICIAATCGATGTCTCGAGAAATAAAGGTTACATGGGGGGTAACTTCCAGGGCACGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCGGTGGACGTAACCCTAGTTTGGACTACGGGTTCAAAGGTGGAGAAATCGCCATGGCTT 1493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCGCTCAATTTTCTGAGCTGGTTAACGATTTCTACAACAATGGATTACCATCGAATCTCT
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                                                                                                                                                                                                                                                         COTATTOTTCCGAGCTTCAATTTTTAGCTAATCCTGTTACCAATCATGTCCAAAGTGCAG
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                                                                                                                                                                       pal4 gene.
Petroselinum crispum.
Petroselinum crispum.
Petroselinum crispum.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                 Expression in Escherichia coli of catalytically active phenylalanine ammonia-lyase from parsley FEBS Lett. 258 (2), 335-338 (1989)
                                                                                                                                                                                                                                                                                                      P.crispum RNA for PAL4, phenylalanine ammonia-lyase
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                                                                                                   Schulz, W., Eiben, H.G. and Hahlbrock, K.
                                                                                                                      Asteridae; euasterids il; Apiales; Apiaceae; Petroselinum 1 (bases 1 to 2375)
                                                                                                                                                              Spermatophyta; Magnoliophyta; eudicotyledons;
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                  1067 CAGTATATTTTGGACGGAAGCGATTACGTCAAGGCGGCGCAAAAGGTCCACGAAATGGAC 1126
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                                                              969 GACCACTTGACACATAAGTTGAAGCATCATCCAGGACAAATTGAAGCAGCTGCTATAATG
                                                                                                                                                                            947 TTST056AA3TSTTATCGGCGATCTTCGCTGAG3TTATGCAA3GGAA3CCGGAA3TTTACC 1006
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                767
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 369 AATAAAGGAACGGATAGTTATGGTGTTACTACTGGTTTTTGGTGCTACTTCTCATAGGAGG
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                                                                                                                                                                                                                                                                                                                               GGAGTTGATAGTGGATTCTTTGAGCTGCAGCCAAAAGAAGGCCTTGCTTTAGTCAATGGC
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                                                                                                         GATCACTTGACACAAATTGAAGCATCACCCTGGTCAAATCGAGGCGGCGGCGATCATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACTAAGCAAGGCGGTGCTTTACAGAAGGAGCTCATTAGATTTTTGGAACGCCGGAATATTC
                                                                                                                                                       TTAGCTGAGGTTATGTCGGCTATATTTGCTGAAGTGATGCAGGGCAAACCTGAATTTACT 968
                                                                                                                                                                                                                                                                   ACCCCCTGGGGTCCGGGATGGCTTCCATGGTCTATTTGATGCTAATGTACTTCCGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOCAMAGCCGTTGGCCCCACCGGAGAAGTCCTCAATGCCGAAAAGGCCTTCGCTGCAGACGCC 826
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GAGAATGATACATTGTCGAACTAGAAGAATAAAGCTTGCAGATCGTACCCGTTGTAT 2086
                                                                                                                                                                                                                                                                                                                          TTTGAAGAAGTGCAAGGCTCTCTTGCCAAAGGAGGTTGAAAGTGCAAGGGCTGTGCTA 1988
                                                                                                                                                                                                                                                                                                                                                       TTCGAAGAAJAATTGAAAGTCCT-TTTACCGAAAGAAGTTGAAGGTGTTAAAATCGCTTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AATCTCTCCGGTGGAACGTAACCCTAGTTTGGACTACGGGTTTCAAAGGTGGAGAAATCGCC 1486
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                                                                                                       AAGTTTATAAGGGAAGAGTTGGGAAA 'AGTTTATTTAAGTGGGTGAGAAGTTGACATCGCCC
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MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TC
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Pflanzenwissenschaften, Eidgenoessische Technische Hochschule,
Zuerich, Universitäetsstrasse 2, 8092 Zurich, SWITZERLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Appert,C., Logemann,E., Hahlbrock,K., Schmid,J. and Amrhein,N. Structural and catalytic properties of the four phenylalanine ammonia-lyase isoenzymes from parsicy (Petroselinum crispum Ny Eur. J. Blochem. 225 (1), 491-499 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
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Astoridae; enastorids II; Apiales; Apiaceae; Petroselinum
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Petroselinum crispum
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                                                                                                                                                                                                NKGTDSYGVTTGFGATSHPPTKQGJALQKELIPELNASITGSGAEAGNNTLPHSATRA
AMLVRINTLIQGYSGIPELLEAITKEINHNITGCLEFGITASGDLVPLSYIAGLL
TGPRNSKAVGPDFGYTLSPELARKAVEGGFBERLGPKEJALVNGTAVGSTANSKULL
TGPRNSKAVGPDFGYTLSPELARKAVEGGFBERLGPKEJALVNGTAVGSTANSKULL
TGPRNSKAVGPDFGYTLSPELARKAVEGGFBERLGPKEJALVNGTAVGSTANSKULL
EANILAVLAEVMSAIFAEVMOGKPEFTDHLTHKIKHHPGQIEAAAIMEHILDGSAYVK
AAQKLIBENDPIQKPKQDRYALIRTSPQMIGDFQIEVIRSSTKMIENEINSVNDNHILDVS
RNKAIHGMNGOGSPIGVSMDNYHLAIAAIGKEKNEAOVSELVNDFYNNGLSENLSSTSKKTSEAVE
TLKLMSTTFLVGLGQAIDLFLANFYINHVUSAEQHNQLVNSLGILSSKKTSEAVE
ELLKMSTTFLVGLGQAIDLFLANFYINHVUSAEQHNQLVNSLGILSSKKTSEAVE
ELLKMSTTFLVGLGQAIDLFLANFYINHVUSAEQHNQLVNSLGILSSKKTSEAVE
ELLKMSTTFLVGLGQAIDLFLANFYINHVUSAEQHNQLVNSLGILSSKKTSEAVE
ELLKMSTTFLVGLGGAIDLFLANFYINHVUSAEQHNQLVNSLGILSSKKTSEAVE
ELLKMSTTFLVGLGGAIDLFLANFYINHVUSAEQHNQLVNSLGILSSKKTSEAVE
ELLKMSTTFLVGLGGAIDLFLANFYINHVUSAEQHNQLVNSLGILSSKKTSEAVE
ELLKMSTTFLVGLGGAIDLFLANFYINHVUSAEQHNQLVNSLGILSSKKTSEAVE
ELLKMSTTFLVGLGGAIDLFLANFYINHVUSAEQHNQLVNSLGILSSKKTSEAVE
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89. .2245
                                                                                                                                                                              PGEEFEKVFTAMSKGEI IDPLLECLESWNGAPLPIC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="mayvngtinghangngldlcmkkedplnwgvaaealigshilbevkmwaeyrkpvvklegeillisovaaisarddsgvkyelseearagykassdwymbsm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="phenylalanine ammonia-lyase
/protein_id="CAA57057.1"
/db_xref="GI:535088"
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/db_xref="taxon:4043"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="SWISS-PROT;P45729"
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Score 12/9.8; DR 8;
Pred. No. 1.1e-293;
0, Mismatches 562;
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1211 1202	GTTATGCTCTCCGTACATCTCCCCAATGGCTCGGACCTCAAATCGAAGTAATCCGATCAT	1152 1143	Qy Db
1151 1142	ACGTCAAGGCGGCGAAAAGGTCCACGAAATGGACCGGTTACAGAAACCAAAACAAGATC	1092 1083	Db Db
1091 1082	ATCACCCTGGTCAAATCGAGGCGGCGGCGATCATGGAGTATATTTTGGACGGAAGCGATT	1032 1023	Оу
1031 1022	TCGCTGAGGTTATGCAASGAAGCCGGAGTTTACCGATCACTTGACACACACAAATTGAAGC	972 963	Оу
971 962	CCATGGTTCTATTTGATGCTAATGTACTTGCGGTTGTTGTCGGAAGTGTTATCGGCGATCT	912 903	Оy
911 902	TACAGCCGAAAGAAGGCTAGCACTTGTTAACGGCACCGCCGTGGGGTCCGGGATGGCTT	852 843	Db Db
851 842	TCCTCAATGCCGAAAAGGCCTTCGCTGCAGCCGGAGTTGAAGGTGGGT 	89 99	Ωу Оф
791 782	CATACATCGCCGGCCTCTTAACCGGCCGCCCAACTCCAAAGCCGTTGGCCCCACCGGAG	732 723	Qy Db
731 722	TCACCCCTTGTTTACCCCTCCGTGGAACCATCACCGCCTCCGGTGACCTTGTCCCATTAT	672 663	Оу
671 662	GTTACTCCGGCATCCGATTCGAGATCTTGGAAGCCATCACCAAGTTCCTTAACAACAACA	612 603	ОУ
611 602	CACTTCCACATTCAGCCACCAGAGCCGCCATGATCGTCAGAATCAACACCCTCCTCCAGG	552 543	Oy Db
551 542	AGCTCATTAGATTTTTGAACGCCGGAATATTCGGCAATGGAACGGAAACAAGCCACA	8 9	ОУ
494 482	CCACCGGCTTCGGCGCCACCTCTCACCGAGAACTAAGCAAGGCGGTGCTTTACAGAAGGCLII	435 423	υğy
434 422	AGGCGAGTAGTGATTGGGTTATGGAGAGCATGAATAAAGGAACTGATAGTTATGGTGTCA	375 363	Qy Db
374 362	CTGCTAATGACAGTGACACCGTGAAGGTGGAGGTGTCGGAGGCGCGGGGGCTTGGAGTTA	315 306	Оу
314 305	AGCCGGTGGTGAAGCTCGGAGGAGAGAGGGTTACAGTTTCTCAGGTGGGGGGATCGCAG	255 246	Оу
254 245	CGGAGGCGTTGACCGGAAGTCACCTTGATGAGGTGAAGAAGATGGTTGCGGAGTTCAGAA	195 186	Oy Db
194 185	ACGITAATGGAGTCGTTAATGAGTTGTGCATCAAGGATCCATTGAACTGGGGAGTTGCAG	135 126	Оу

Qy Qy	Db Qy	Db 40	2 P	рь Оу	Db Oy	ОУ	ОУ	Qу	Ωy	Qy Db	Qy Db	Суу	Qy Db	Qу	Qу Пъ	Qy Db
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GGAACCTCTTCCANTATGTTAGGAAAGTGAGTGGAAACCGTTTGAATTGTATTGTAA 2291	ດ – ດ ;	ACAGGATTAAGGAGTGCAGGTCTTACCCTCTGTACAAGTTTTGTGAGGGAAGAATTGGGAA 2102 GAGGGTTTTGACCGGAGAAAAGGTGACGTCGCCGGGAGAGGAGTTCGACAGGGTGTTCA 2171	TGCCTAAAGAAGTCGAAACTGCTAGAGCCGCACTTGAAAGTGGAAATCCGGCAATCCCCA 2042 ACAGGATTAAAGCTTGCAGATCGTACCCGTTGTATAGGTTTGTAAGGGAGGAGCTCGGCA 2111	ACTTGAGCACTTCCATCTCCAAAAGATTGCAGCATTCGAGGATGAGACTAAAGGCTCTTC 1982 TACCGAAAGAAGTTGAAGGGTGTAGAATGCCTTATGAGAATGAAAGAATGCAATCCAA 2051	TICHARAGETICCHAE'AGGTECTGEFFCSACCACGCTCTAAACAACACGGGAAACACGGAGAAGA 1931		TGGGCGTCAACGGCGAGCTCCACCCGTCGAGATTCTGCGAGAAAGATCTCCTCCGTGTTC 1811 	AGAACATGAAATCGACAGTGAAGAACACCGTAAGCCAAGTCGCGAAAAAGGTCCTCACCA 1751 	TCATGTCGICGACATACTIAGTCGCTCTATGCCAATCCATCGATTTACGCCATTTGGAAG 1691	TTAATTCTCTCGGATTAATTTCAGCGAGGAAAACCGCAGAAGCAGTCGACATCTTAAAAC 1631 	AGTTTCTCGCAAATCCAGTCACTAACCATGTTCAAAGCGCGAACAACAACAATCAAGACG 1571 	GTTTGGACTACGGGTTCAAAGGTGGAAATCGCCATGGCTTCTTACTGTTCTGAGCTTC 1511	TGGTTAACGATTTCTACAACAATGGATTACCATCGAATCTCTCCGGTGGACGTAACCCTA 1451 	ACAACACCCGTCTCGCCATTGCTGCAATCGGAAAACTCATGTTCGCTCAATTTTCTGAGC 1391 	CCAGAAACAAAGCTTTACACGGTGGTAACTTCCAAGGAACCCCAATCGGAGTTTCCATGG 1331 	CAACCAAAATGATCGACAGGGAAATCAATTCCGTCAACGACAACCATTGATCGACGTTT 1271

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Kim,J.-B., Kim,J.-B., Cho,K.-J., Woon,U. and Ha,S.
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/trans!ation-"MAANGHRGSNGHNNGANGFCVKONDPLNWAAAAESLKGSHWVNDSMS
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RESULT 7
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                                                                                                     REFERENCE
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                                                                                                                                                                                                                                                                                                       KEYWORDS
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                                        TITLE
                                                                                                                                                                                                                                      ORGANISM
                                                                       AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2138 GGGGAGGAGTGCGAGAAGGTGTTCGCGGCGTTGAGCAATGGCCTCATTATTGATCCATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1787 TGCGAGAAAGATCTCCTCCGTGTTGTTGATCGTGAATACGTCTTCGCTTACATCGACGAC 1846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1427 AATCTCTCCGGTGGACGTAACCCTAGTTTGGACTACGGGTTCAAAGGTGGAGAAATCGCC 1486
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2018 GAGAGTGGGAGTCCGGCTGTGGCGAACCGGATTGAGGAATGCCGGTCGTTCCCCTGTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2027 GAGAATGATACATTGTCGATTCCAAACAGGATTAAAGCTTTGCAGATCGTACCCGTTGTAT 2086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1958 TTCGAGGAGGAGCTGAAGGCCCTGCTACCCAAGGAGGTCGAGAGCGCAAGGATCGCCCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1838 CCCTGCCTCGCGACCTACCCGTTGATGCAGAAGCTGAGGCAGGTGCTGGTCGACCACGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1778 TGCGAGAAGGAACTCATCCGCGTTGTCGACCGTGAGTACGTGTTCACCTACATTGACGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1658 GCCGTCGATCTGAGGCATGTGGAGGAGCATGAAGCTCGCCGTGAAAAACACTGTCAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2087 AGGTTTGTAAGGGAGGAGCTCGGCAGAGGGTTTTTTGACCGGAGAAAAAGGTGACGTCGCCG 2146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTGGAGTGTCTTGGAGGGTGGAATGGGGAACGTCTTCCAATATGTTAG 2254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGCGCCGAACAACAATCAAGACGTTAATTCTCTCGGATTAATTTCAGCGAGGAAAACC 1606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTGGAATGCCTTCAAGGATGGAATGGTGAACCTCTGCCTATCTGCTAC 2245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGCGCGGAGCAGCACCAGGATGTTAACTCACTAGGGTTAATCTCCTCGCGCAAGACG 1597
                                                         Asteridae; euasterids I: Solanales; Solanaceae; Nicotiana I (bases 1 to 2462) Pellegrin, L., Rohfritsch, O., Fritig, B. and Legrand, M.
   expression during the hypersensitive reaction to tobacco mosaic
                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
                                                                                                                                                                                                                                Nicotiana tabacum
                                                                                                                                                                                                                                                                  Nicotiana tabacum.
                                                                                                                                                                                                                                                                                                    phenylalanine ammonia-lyase
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                                                                                                                                                                                                                                                                                                                                                                                                                                           NTPHEAL
                              Phenylälänine ammonia-lyase in tobacco. Molecular cloning and gene
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444 CTGGTTTTGGTGCTACTTCACATAGGAGAACCAAGAACGGTGGTGCTCTTCAAAAGGAAC
                                     438 CCGGCTTCGGCGCCACCTCTCACCGGAGAACTAAGCAAGGCGGTGCTTTACAGAAAGGAGC
                                                                                                                             384 CTAGTAGTGATTGGGTTATGGATAGTATGAGTAAAGGAACTGATAGTTATGGTGTTACTA
                                                                                                                                                                                                                                                              324 AAGATAATGCTAAAACTGTAAAAGTGGAGCTTTCTGAAGGAGCAAGAGCTGGTGTTAAAG
                                                                                                                                                                                                                                                                                                                                                                                            264 CAGTAGTGAAACTTGGAGGTGAGACTTTAACAGTGGCACAAGTTGCGGCTATTGCTGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                204 ATTCATTGAAAGGAAGCCATTTAGATGAAGTGAAGAAAATGGTGGCTGAGTTTAGGAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              144 GTCACCAAGAAATGGATTTTTGCGTTAAAGTGGATCCATTGAACTGGGAAATGGCAGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        141 ATGGAGTCGTTAATGAGTTGTGCATCAA---GGATCCATTGAACTGGGGGGGTGCAGCGG
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                                                                                                                                                                      CGAGTAGTGATTGGGTTATGGAGAGCATGAATAAAGGAACTGATACTTATGGTGTCACCA
                                                                                                                                                                                                                                                                                                                               CTAATGACAGTGACACCGTGAAGGTGGAGCTGTCGGAAGCCGCGAGGGCTGGAGTTAAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 virus and the response to a fungal elicitor Plant Physiol. 106 (3), 877-886 (1994) 95125127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7824656
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VFSEVLSAIFAEVMNGKPEFTDHLTHKLKHHPGOIEAAAINEHLLDGSSYVKAPOKLH
ETDPLQKPKQDRYALTTSPQWLGPLEVIRASTKMIEREINSVNDNPLIDVSRNKALH
GGNEGGTPIGVSMDNARLALASIGKLMFAQFSELVNDYYNNGLPSNLTAGRNPSLDYG
FKGSEIAMASYCSELQFLANPVTNHVQSAEQHNQDVNSLGLISARKTAEAVDILKLMS
STYLVALCQAIDLRHLEENLRNAVKNTVSQVAKRTLTMGANGELHPSRFCEKDLLRVV
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SYGVTTGFGATSHRRTKNGGALQKELIRFLNAGVFGNGTESCHTLPQSGTRAAMLVRI
NTLLQGYSGIRFEILEAITKLLNHNVTPCLPLRGTITASGDLVPLSYIAGLLTGRPNS
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/protein_id="CAA55075.1"
/db_xref="GI:633597"
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/clone_lib="Lambda ZAP II vector, cDNA from tobacco leaves
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VLPKEVESARISLENGNPAIANRIKECRSYPLYRFVREELGAELLTGEKVRSPGEECD
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/translation="MAGVAQNGHQEMDFCVKVDPLNWEMAADSLKGSHLDEVKKMVAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="PAL.E"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Nicotiana tabacum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /EC_number="4.3.1.5"
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                                                                                                                 TTCAACTGTGCTGTATGTGGTTGTAAATCATATATATTAACTTATTATTTTTGCTAAAAA 2417
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AAATGAAAAGTGACAA 2435
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RESULT 8
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ACCESSION VERSION SOURCE KEYWORDS DEFINITION CMEPAL 2330 bp mRNA linear PLN 06-FE Camellia sinensis mRNA for phenylalanine ammonia-lyase (PAL),

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phenylalanine ammonia-lyase; PAL. Camellia sinensis (cultivar:Yabukita) young leaf cDNA to mKNA, D26596 1 GI.662270 complete cds.

PLN 06-FEB-1999

clone_lib:lambda gtll clone:A21.
Camellia sinensis Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

ORGANISM

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TITLE
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480 CATAGGAGGACCAAAGAAGGTGGTGCTCTTCAAAAGGAGCTTATTAGGTTCTTGAATGCT 539
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                                     CACCGGAGAACTAAGCAAGGCGGTGCTTTACAGAAGGAGCTCATTAGATTTTTGAACGCC
                                                                                                  GAGAGCATGAATAAAGGAACTGATAGTTATGGTGTCACCACCGGCTTCGGCGCCACCTCT
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                                                                                                                                                                                                                                                                                                                                                                                                    TTTTGTCTGAAAGACCCTTTGAATTGGGGAGTGGCGGCGGAGGCAATGAAGGGGAGTCAT 245
                                                                               GAGAGTATGAATAAAGGGACAGATAGTTATGGTGTTACTACTGGTTTTTGGTGCTACTTCA
                                                                                                                                                                                                   AACGTGGAGCTCTCGGAAGCCCGCGAGGGCTTGAGGTTAAGGCCGAGTAGTGATTTGGGTTATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (22-JAN-1994) Satoru Matsumoto, Natl. Res. Inst. Vegetables, Ornamental Plants and Tea; Kanaya 2769, Kanaya, Shizuoka 428, Japan (Tel:0547-45-4101, Fax:0547-46-2169)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Spermatophyta; Magnoliophyta; eudicotyledons, core eudicots. Asteridae; Ericales; Theaceae; Camellia.
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MVEEFRKPVVRLGGETLTISGVAAIAVRGSEVAVELSESAGVKASSDWYMESMNKG
TDSVGVTTGFGATSHRRTKEGGALQKELIRFLNAGIFGNGTESCHTLPGSATRAAMLV
RINTLLQGYSGIRFEILEAISKFLNNNITPCLPLRGTITASGDLVPLSYIAGILTGRH
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LHEMDPLOKPKODRYALRTSPOMLGPL I EV I RSSTKS I ERE I NSVNDNPL I NVSRNKA
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Ş 1598 AGGAAAACCGCAGAAGCAGTCGACATCTTAAAACTCATGTCGTCGACATACTTAGTCGCT 1657 1260 AACTCGGTGAATGACAACCCTTTGATCAATGTTTCAAGGAACAAGGCCTTACATGGTGGA 1319 1118 GAAATGGACCCGTTACAGAAACCAAAACAAGATGGTTATGCTCCCGTACATCTCCCCAA 1177 1080 GCCATTATGGAACATTTTGGATGGTAGCTCTTATGTCAAGGCAGCCCAAAAACTACAT 1139 938 CTTGCGTTGTTGTCGGAAGTGTTATCGGCGATCTTCGCTGAGGTTATGCAAGGGAAGCCG 540 GGAATATTTGGCAATGGAACAGAGTCATGTCACACATTGCCACAATCAGCCACAAGGGCA TGGCTCGGACCTCAAATCGAAGTAATCCGATCATCAACCAAAATGATCGAGAGGGAAATC 1237 GAGTTCACCGACCATTTGACACACAAATTGAAGCACCACCCTGGCCAAATTGAAGCTGCT 1079 CATGTCCAAAGCGCCGAGCAACATAACCAAGATGTGAACTCTTTAGGCCTAATCTCTTCA CATGTTCAAAGCGCCGAACAACAACAATCAAGACGTTAATTCTCTCGGATTAATTTCAGCG 1597 GAGATTGCCATGGCTGATTGCTCAGAACTCCAATTCCTTGCCAATCCTGTAACCAAC GAAATCGCCATGGCTTCTTACTGTTCTGAGCTTCAGTTTCTCGCAAATCCAGTCACCAAC 1537 TTACCATCAAATCTTTCCGGGGGGACGAAATCCAAGTTTGGATTATGGTTTCAAGGGAGCC TTACCATCGAATCTCTCCGGTGGACGTAACCCTAGTTTGGACTACGGGTTCAAAGGTGGA 1477 ATAGGGAAGCTCATGTTTGCCCAATTCTCTGAGCTTGTTAATGACTTCTACAACAATGGG ATCGGAAAACTCATGTTCGCTCAATTTTCTGAGCTGGTTAACGATTTCTACAACAATGGA 1417 AATTTCCAAGGTACCCCAATCGGAGTCTCCATGGACAATACACGTCTAGCTGTTGCCTCA TGGCTAGGACCACTAATTGAAGTCATCCGATCATCGACAAAATCAATTGAGAGGGAGATA 1259 GAAATGGATCCATTGCAAAAACCAAAACCAAAACAGGACAGATATGCCCTTAGAACATCTCCTCAA GCGATCATGGAGTATATTTTGGACGGAAGCGATTACGTCAAGGCGGCGCAAAAGGTCCAC GAGTTTACCGATCACTTGACACACAAATTGAAGCATCACCCTGGTCAAATCGAGGCGGCG CTCGCCGTGTTATCAGAAGTTTTGTCAGCGATTTTCGCTGAAGTTATGCAAGGCAAGCCC GTCAACGGCACAGCTGTTGGTTCCGGGCTTGGCTTCTATGGTTCTTTTCGAGGCTAACATA GCTGCAGCCGGAGTTGAAGGTGGGTTCTTCGAGTTACAGCCGAAAGAAGGCCTAGCACTT CGGCACAATTCGAAGGCGGTCGGGGCCTACTGGAGAAATCCTCCACCCCAAGGAAGCCTTC CGCCCCAACTCCAAAGCCGTTGGCCCCACCGGAGAAGTCCTCAATGCCGAAAAGGCCTTC ACTATCACCGCCTCCGGTGACCTAGTCCCCCTATCTTACATTGCCGGGCTTTTGACAGGC ACCATCACCGCCTCCGGTGACCTTGTCCCATTATCATACATCGCCGGCCTCTTAACCGGC GCTATGCTTGTAAGGATCAACACCCTCCTCCAAGGATACTCCGGCATTAGGTTCGAAATT 659 GCCATGATCGTCAGAATCAACACCCTCCTCCAGGGTTACTCCGGCCATCCGATTCGAGATC AACTTCCAAGGAACCCCAATCGGAGTTTCCATGGACAACACCCGTCTCGCCATTGCTGCA 1357 AATTCCGTCAACGACAACCCATTGATCGACGTTTCCAGAAACAAAGCTTTACACGGTGGT 1297 GTTAACGGCACCGCCGTGGGGTCCGGGATGGCTTCCATGGTTCTATTTGATGCTAATGTA TTGGAAGCCATCACCAAGTTCCTTAACAACAACATCACCCCTTGTTTACCCCCTCCGTGGA 1619 1559 1499 1439 . 1379 1019 1057 997 697 937 877 839 817 757 899 779

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         Submitted (25-AUC-1993) Mitsuo Okazaki, Faculty of Textile Science and Technology, Shinshu Univ., Department of Applied Biology; 3-15-1 Tokida, Deda, Nagano 386, Japan (Tel.0286-22-1215(ex.255).
                                                                                                                                                                          Cloning and sequencing of a full-length cDNA coding for phenylalanine ammonia lyase from tobacco cell culture plant physicl. 104 (3), 1091-1092 (1994)
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D17467.1 GI:2570155
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                                                                                      Direct Submission
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Fax:0268-22-4079)
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Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   193 - АĞСЫЗАĞĞСЫТТҚАССЫЗААĞТСАССТТҚАТҚАҚЫТҚААҚААҚАТБЫТҚЕСЫҚҚІТТСАҚ - 25 2
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ETDPLQKPKQDEVALTTSPQMLGPQIEVE FRATKMIEREINSVUNDPLLDVSRUKALH
GGNEGGT PIGVSMDUNKLALAASIGKLMFGOFSELVNUY VNNILPSNLTAFARNESLDYL
EKOSEIAMASYCSELQFLANPVTNIIVOSAEGINODVNSLDLISARKTAEAVDILKLMS
STYLVALOQAIDLEHLEENLENAVKNIIVSOVAAKTILMGINGELHPSWECEKDLIKVV
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NTLLQGYSGIRFEILEAITKILNHNVTPCLPLRGTITASGDLVPLSYIAGLLTGRPNS
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/db_xref="GI:2570156"
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1633 CATGTCGTCGACATACTTAGTCGCTCTATGCCAATCCATCGATTTACGCCATTTGGAAGA 1692
                                                                                                                                                                                                                                                                                                                                 1453 TTTGGACTACGGGTTCAAAGGTGGAGAAATCGCCATGGCTTCTTACTGTTCTGAGCTTCA 1512
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                                                      1662 GAACTCCTTGGACTTAATCTCAGCTAGAAAAACAGCTGAAGCCGTGGACATCTTAAAGCT 1721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1213 AACCAAAATGATCGAGAGGGAAATCCAATTCCCTCAACGACAACCCATTGATCGACGTTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGGGTTTTTGACCGGAGAAAAGGTGACGTCGCCGGGAGAGGAGTTCGACAGGGTGTTCAC 2172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAGGATAAAAGAATGCAGATCTTATCCACTTTACAGGTTTGTTAGAGGAGAACTTGGAGC
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                                                         Unpublished
                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Gentianales; Apocynaceae; Rauvolfioideae;
Direct Submission
                       Kiyota, S
                                                                                           cDNA of phenylalanine
                                                                                                                           Kiyota, S
                                                                                                                                                                          Vinceae; Catharanthus.
                                                                                                                                                                                                                                                                         Catharanthus roseus
                                                                                                                                                                                                                                                                                                Catharanthus roseus cDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                     AB042520.1 GI:7798553
                                                                                                                                                                                                                                                                                                                                                                                                                         AB042520 2495 bp mKNA linear PLN 12-MAY-200 Catharanthus roseus mRNA for phenylalanine ammonia lyase, complete
                                         (bases 1 to 2495)
                                                                                                                                             (sites)
                                                                                                                           Sakano, K. and Kim, J
                                                                                                 ammmonia lyase from Catharanthus roseus
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                                                                                       GTTCCTTAACAACAACATCACCCCTTGTTTACCCCTTGGTGGAAACCATGACGACGCCTCCGG 714
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                                                                                                                                                                                                                                                                                                                                                                                                     AGGCGGTGCTTTACAGAAAGAGCTATATAGATTTTTGAACGCCGGAATATTCGGCCAATGG 534
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                                                                                                                                               CAACACCCTGCTTCAAGGTTACTCCGGGATCAGATTTGAGATCCTAGAAGCCATTACCAA 694
                                                                                                                                                                                                                                                        AACAGAATCTTCCCACACACTGCCACACTCAGCAACGAGGGGCTGCAATGCTCGTGAGAAT
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                                                                                                                                                                                                                                                                                                                                                                       AGGCGCTGCTTCAGAAGGAGCTTAFTAGGTTTCTGAATGCTGGAATCTTTGGGGAATGG
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KGTUSYGVTTGFGATSHKFTKQGGALQKELIFFLNAGIFGNGTESSHTLPHSATRAAM
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NTLAVLSEVLSATFAEVMNGKPEFTDHLTHKLKHHPGQTEAAATMEHTLDGSGYVKAA
HKLHEMDPLOKPKQDRYALRTSPOWLGPQTEVTRSATKMTERETNSVNDNPLLDVSRN
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                                                                                                                                                                                                                                                                                                       CGGTGGACGTAACCCTAGTITGGACTACGGGTTCAAAGGTGGAGAAATCGCCATGGCTTC 1494
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                                                       AAAGAGAACTOTAACCGTTGGTGAATGGAATGGAACTTGATGATGAAGATTTTGCGAAGAA
                                                                                                                                                                   TITITGAGGCATTITIGGAGGAGAACTTGAAAAATGCAGTGAAAAACACAGTTAGCCAAGTTIGC
                                                                                                                                                                                                                     TTTACGCCATTTGGAAGAGAAGAACATGAAATCGACAGTGAAGAACACCGTAAGCCAAGTCGC
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                                                                                                        5'UTR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAACCCGGCAATCCCTAACCGGATCAAGGAATGCAGATCATATCCGTTGTATAAGTTTGT
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                                                                                                                                                                                                                                                                                                                                                                  Manners, J.M., McIntyre, C.L. and Nourse, J.P. Cloning and sequence of a cDNA encoding phonylalanine ammonia-lyase from the tropical forage legume stylosanthes humilis plant Physiol. 108 (3), 1301-1302 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trachcophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        phenylalanine ammonia-iyase Stylosanthes humilis.
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                                                             /gene="PAL17.1"
32. .2179
                     /gene-"PAL17.1"
/EC_number="4.3 1.5"
/codon_start-1
                                                                                                                         /gene-"PAL17.1"
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                                                                                                                                                                                      /tissue_type="stem"
1. .2428
                                                                                                                                                                                                                            /db_xref="taxon:35628"
                                                                                                                                                                                                                                                /strain="Paterson"
                                                                                                                                                                                                                                                              /organism="Stylosanthes humilis"
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                                                                                                   693 CCAAGGCTGTTGGACCCAATGGAGAGACTCTTAATGTAAAGGAAGTATTCCAAGCCGCCG
                                                                                                                                          768 CCAAAGCCGTTGGCCCCACCGGAGAAGTCCTCAATGCCGAAAAGGCCTTCGCTGCAGCCG
                                                                                                                                                                                                                        708 COTOCGGTGACCTTGTCCCATTATCATACATCGCCGGCCTCTTAACCGGCCGCCCCAACT
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                                                             GAGTIGAAGGTGGGTTCTTCGAGTTACAGCCGAAAGAAGGGGCTAGCACTTGTTAACGGCA 887
                                                                                                                                                                                                                                                                   TAACCAAGCTTCTCAACAACAACATTACACCCTGTTTTGCCACTTAGGGGGAACAATCACAG
                                                                                                                                                                                                                                                                                                         TCACCAAGTTCCTTAACAACAACATCACCCCTTGTTTACCCCCTCCGTGGAACCATCACCG
                                                                                                                                                                                                                                                                                                                                                 TGAGGATCAACACACTCCTCCAAGGCTACTCAGGAATCAGATTTGAGATCTTGGAAGCCA
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692 767 632 707

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219 CTATATCTCAGGTGGCCGCCATTGCTGCTAACGACCAAGGCGTCTCC-----GTTCAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             228 TGAAGAAGATGGTTGCGGAGTTCAGAAAGCCGGTGGTGAAGCTCGGAGGAGAGACGCTTA 287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
GCAATGGTACAGAGACAAATTGCCACATTGCCACACACAGCTACTAGAGCAGCAATGCTAG
                                                                GCAATGGAACGGAAACAAGCCACACATTCACATTCAGCCACCAGAGCCGCCATGATCG
                                                                                                                                            CCAAACAGGGCGGTGCCTTGCAGAAAGAGCTCATTAGGTTCTTGAATGCTGGAATATTTG
                                                                                                                                                                                                                CTAAGCAAGGCGGTGCTTTACAGAAGGAGCTCATTAGATTTTTGAACGCCGGAATATTCC
                                                                                                                                                                                                                                                                                        ACAATGGTACCGACAGCTATGGTGTCACCACCGGCTTTGGCGCCACTTCTCACCGCAGAA
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ALHGGNPGGTPIGVSMDNTRLAVASJCKLAPSTSHVDFYNNGL/PSNLSASRNPSL
DYGFKGTEIAMASYCSELQYLANPVTSHVQSAEQFSHLVNDFYNNGL/PSNLSASRNPSL
LMSPTYLIALCQAIDLRHLEENLKNTVKNTVSQVAKRTLTTGVNGELIESRFCEKDLL
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/gene="PAL17.1"
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ECDKLFTAMCQGKTIDPLLECTGEWNGAPLPLC"
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ILAVLSEVLSAIFAEVMOGKPEFTDHI.THKLKHHPGQIEAAAIMEHII.DGSSYVKAAK
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GTDSYGVTTGFGATSHRRTKQGGALQKELIRFLNAGIFGNGTEINCTLPHTATRAML
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/db_xref="G1:55642"
/translation="MDTHANADATFCLTANNGOOPRHDPLNWAAAAFALKGSHLDEVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            535 c
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                                                                                                                                                                                                                                                                                                                              GCGAGAAAGATCTCCCTCCCTCTTTGTTGATCGTTGAATACGTCTTTCGCTTACATCGACGACG
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                                                          TTGCAAATGCTGAAAATGAGAAGAATGTGAAACACCTCAATCTTCCAGAAAATTACAACCT
                                                                                                               TAMACANCGG GAAACGGAGAAGAACACTAACACCTCCATCTTCCAAAAGATCGCTACCT 1967
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2073 GTGAAGAATGTGACAAATTGTTCACGGCAATGTGGCCAAGGCAAGATCATTGATGCTCTTC
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NILLDGYSGIRFEILETITKFLNHNITPCLPLRGTITASGDLVPLSYIAGLLTGRPNS
KAVGPNGESLNAEQAFKLAGANSGLFFELQPKEGIALVNGTAVGSGLASIALYEANTIL
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ORIGIN BASE COUNT Matches 1629; Conservative Query Match 1015 ACTGATCACCTGACGCACAAGTTGAAGCATCACCCGGGCCAAATAGAGGCAGCCGCTATA 1074 1004 ACCGATCACTTGACACACAAATTGAAGCATCACCCTGGTCAAATCGAGGCGGCGGCGATC 1063 167 AAGGATCCATTGAACTGGGGGGGTTGCAGCGGGAGGCACTCACCTTGATGAG 226 715 GCATCAGGCGATCTCGTGCCCTTATCCTACATCGCAGGCCTCTTAACGGGTCGGCCCAAC 774 655 ATCACCAAATTCCTCAATCACAACATCACCCCATGCTTGCCCCTCCGCGGGACCATAACC 475 ACGAAACAAGGCGGTGCTCTTCAGAAGGAGCTTATTAGGTTCTTGAACGCCGGAATATTC 534 415 AACAAAGGGACTGACAGCTATGGCGTCACCACGGGATTTGGTGCCACGCTCACACCGCAGG 347 CTGTCGGAAGCCGCGAGGGCTGGAGTTAAGGCGAGTAGTGATTAGGGTTATTGGAGAGCATG 406 181 AATGATCCCTTGAACTGGGTGGCGGCGGCGGAGGAGCTGAAGGGGAGCCATCTGGATGAG 240 955 TIGTIGGCTGAAGIGATGTCCGCCGTTTTTGCAGAGGTAATGAACGGAAAGCCCGAATIC 1014 944 TTGTTGTCGGAAGTGTTATCGGCGATCTTCGCTGAGGTTATGCAAGGGAAGCCGGAGTTT 1003 895 GGGACAGCTGTTGGGTCCGGATTGGCCCTCAATTGCCCCTTTATGAAGCGAACATCCTTTCC 767 TCCAAAGCCGTTGGCCCCACCGGAGAAGTCCTCAATGCCGAAAAGGCCCTTCGCTGCAGCC 647 ATCACCAAGTTCCTTAACAACAACATCACCCCTTGTTTACCCCTTCCGTGGAACCATCACC 535 GGAAATGGGACAGAATCTACGCACACACTGCCACATTCAGCAACCAGAGCAGCAATGCTT 594 527 GGCAATGGAACGGAAATAAGCCATACACTTCCACATTCAGCCACCAGAGCCGCCATGATC 586 467 ACTAAGCAAGGCGGTGCTTTACAGAAGGAGCTCATTAGATTTTTGAACGCCGGAATATTTC 407 AATAAAGGAACTGATAGTTATGGTGTCAUCAUUGGCTTCGGCGCCACCTCTCACCGGAGA 466 355 CTGGCGGAGTCATCGCGTGCTGGGGTGAAGGCCAGCAGTGATTGGGTGATGGAGAGCATG 301 ACGATATCTCAGGTGGCGGCGATCGCCGCTAGGGA-----CAATGAGGTGGCCCGTGCAG 354 241 GTGAAGCGGATGGTGGAGGAGTTCAGGAAGACAGTGGTGAAGCTCGGCGGCGAGACTCTG 300 Local Similarity GGAG---FIGAAGGTGGGTTCTTCGAGTTACAGCCGAAAGAAGGCTTACCACTTGTTAAC 883 GGCACCGCCGTGGGGTCCGGGATGGCTTCCATGGTTCTATTTGATGCTAATGTACTTGCG 943 TCCAAGGCCGTGGGGCCCAACGGCGAGTCCCTCAATGCGGAACAAGCATTCAAGCTTGCC GTGAGAATTAACACCCTCCTCCAGGGATACTCCGGCATCAGATTTGAAATCTTGGAAACC GTCAGAATCAACACCCTCCTCCAGGGTTACTCCGGCATCCCGATTCGAGATCTTGGAAGCC 646 GGTGCCAATTCCGGATTATTCTTCGAGTTGCAGCCGAAAGAAGGCCTCGCCCTCGTGAAC GCCTCCGGTGACCTTGTCCCATTATCATACATCGCCGGCCTCTTAACCGGCCGCCCCAAC ACAGTTTCTCAGGTGGCGGGGATCGCAGCTGCTAATGACAGTGACACCGTGAAGGTGGAG GFKGSELAMASYCSELGFLARIPTINHVQSAEQHNODVNSLGLISSRKTYBALDIIKLM SSTYLVALCQALDLPHLEENLRLSVKITISQVAKRTLTTISVNIŞELHPSPFF ELGLLPV VDREYVFAYVUDDCSATYPLMQKLQVKIVISQVAKRTLTTISVNIŞELHPSPFF ELGLLPV AVLPKEVVESARVALEDGKPAJANRITECRSYPLYKFIREELGTNFLTGEKVMSPGEEC DRVF"TAMSKGLIVDPLLKCLEGWNGAPLPIC" 50.6%; 73.1%; 549 c 0; Mismatches 590; Indels Score 1235; DB 8; Pred. No. 4.2e-285; 628 g Length 2403; 10; Caps 474 834 ω

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Вb QΥ DЬ 9 Dβ QΥ В Qγ Ъ Ę рЬ γQ B Qy 밁 Qy Дb Qy Ър δÃ 밁 200

δÃ 밊 Ş. Вb Qy Пþ δδ Дb

1064 ATGGAGTATATTTT95A095AA0903ATTACGTCAA030GGGCAAAAGGTCCACGAAATG 1123

DECEMBER DECEMBER																																			
124 GACCGGTTACAAAACCAAAACAAATCATTATTATTATTCAGGAAATTCATTC	43	Db	Qy	Фy	В	ŶΫ	DЬ	Оу	Db	Qy	Ъ	Qy	рb	Qy	Db	Qy	Db	Qy	Db	Qy	DЪ	Qy	Вb	Оу	Dр	Qy	Db	Qy	Db	Qy	da	Qy	qq	QY	둥
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2215 TEGTTGAAGTGTCTTGAGGGGTGGAAGGGTGCACGTGTTTGCTATCTGCTAGGTGCATTATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2155- ООМБЕБЯМБЭЛАТЫТЫМ МЕНЕТЕТТ МЕБЕР АЛТЫК УАЛМЕРУ ТЕЛІТТЕТТЕЛТЕСА. 2214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2204 TTGTTGGAGTGTGTTGGAGGGTGGAATGGGGAACCTCTTCCAATATGTTAGGAAAGTGAG 2263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGACTACAT 2402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (09-DEC-1995) Yoshiyuki Tanaka, National Institute of Agrobiological Resources, Applied Physiology, 2 1 2 Kannodal, Tsukuba, Ibaraki 305, Japan (Tel:0298-38-8376, Fax:0298-38-8347)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheo
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Convolvulaceae; Ipomoea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ipomoea batatas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ipomoea batatas (strain:beniazuma) wounded root cDNA to mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xrei="taxon:4120"
/clone="pAL2-8"
/tissue_type="wounded root"
87, .2213
                                                              AVCDGG11DPLLECLKSWDGAPLPIC"
1 594 c 604 g 595 t
                                                                                                                                                             LOKPKODRYALKTSPOWLGPO LEV LROATKMLEHE LNSVNDNPLLIDVSRNKALHGGNF
OGTP LGVSMDNSRLALAS LGKLLFAOF SELVNDYYNNGLPSNLTAGRNPSLDYGFKGV
ELAMASYCSELOFLANPYTNHVOSAEOHNODVNSLGLLSARKTAEAVDVLKLMSSTYL
                                                                                                                    VALCQAIDLRHLEENLKNAVRNTVNQVAKRTLTMGVNGELHPSRFCEKDLLRVVDREY
VFAYADDPCSANYPLFQKLRQVLVDHALQNGEHEKNVSTSIFQKIAAFEDELKAVLPK
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TTGFGATSHRRTKNGHALQQELL I RFLNAG I FGTGTGASHTLPHSATRAAMLVR I NTLL
                                                                                                                                                                                                                                                                                                                           /product "Phenylalanine Ammonia-Lyase"
/protein_id-"BAA11459.1"
/protein_id-"BAA11459.1"
/db_xref-"GI:1122743"
/translation-"MEGAIANGHTNUFCIKVUPF.NWEMAADSLKGSHLDEVKRMVAFF
                                                                                                     EVEGARSATENGNPATPNRTTECRSYPLYKEVREELGTEMLTGEKVKSPGEVCDKVFT
                                                                                                                                                                                                                          VLSAIFAEVMNGKPEFTDHLTHKLKHHPGQIEAAAIMEHILDRSYYMKAAQKLHEMDP
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  Score 1231.4;
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Best Local Similarity
                        1157 GUTUTOUGTACATOTOUCCAATGGCTOGGAQUTUAAATGGAAGTAATOUGATGAFQAAGO
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                                                                                                                                                                                                          CCTGGTCAAATCGAGGGGGGGGGATCATGGAGGAGTATATTTTGGAGGGAAGCGATTACGTC 1096
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                                                                           AAGGCTGCACAGAAACTGCACGAAATGGATCCATTGCAGAAAGCCCAAACAAGATCGTTAT 1115
                                                                                                                                                                                                                                                                                 GARATRATRAATRAARARATTTACCGACCATTTGACTCATAAGCTGAAGCATCAT 995
                                                                                                                                                                                                                                                                                                                                 GAGGITTATGCAAGGGAAAGCGGGAGITTACCGATCACTTGACACACAAAATTGAAGCATCAC 1036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONTRACTSCOTCTCCGTGGCA/CAATCACCGCCTCCAGIGACCITGTGCCIIIATCCTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCTCACTCAGCTACAAGGGCAGCTATGCTTGTGAGGATCAACACTCTTCTTCAAGGATAC 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTCATCAGGITCTTGAATGCIGGAATITITGGGACTGGAAGCAGGGGCAAGCCACACACTA 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCGAGTAGTGATTGGGTTTATGGAGAGGCATGAATAAAGGAAACTGATAGTTATGGTGTCACC 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCTAATGACAGTGACAGGGGAAGGTGGAAGTTGTGGAAGGCGGGGAGGGCTGGAGTTAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCGGTGGTGAAGCTCGGAGAGAGAGACGCTTACAGTITCTCAGGTGGGGGGGGGAICGCAGCT 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GACTCATTGAAGGGGGGGGACTTGGATGAAGTGAAGTGCATGGTGGCGGGAGTTGAGGAAC 224
                                                                                                                               AAGGCGGCAAAAGGTCCACGAAATGGACCCGTTACAGAAACCAAAACAAGATCGTTAT 1156
                                                                                                                                                                             CCTGGTCAAATTGAGGCTGCTGCTATAATGGAACATATTTTGGATAGAAGCTATTACATG 1055
                                                                                                                                                                                                                                                                                                                                                                                        GTTCTGTTTGAGGCTAATGTTCTTGCGGTGTTGTCTGAGGTTTTGTCTGCAAATTTTCGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                      GTICTATITGATGCTAATGTAGTTGCGTTGTCGGAAGTGTTAICGGCGATCTICGCT 976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCTAAGGAAGGGCTTGCACTTGTGAATGGAACTGCTGTGGGGTTCTGGGCATGGCGTCTATG 875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCGAAAGAAGGGCTAGCACTTGTTAACGGCAACCGCGTGGGGGTCCGGGGATGGCTTCCATG 916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATCGCCGGCCTCTTAACCGGCCGGCCCAACTCCAAAGCCGTTGGCCCCACCGGGAGAAGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACTUBECTTCGGCGCCACCTCTCACCGGAGAAACCAAGAACGGCCATGCTCTTCAGCAGGAG
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Conservative
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0; Mismatches 551;
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                                                                          2237 CCTCTTCCAATATGTTAGGAAAGTGAGTGTGAAACCGTTTGAATTGTAATATTC 2296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1716
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                                                                                                                                                                                                                                                                                                                                                          ATGCTGACCGGAGAGAAGGTGAAGTCGCCGGGAGAAGTGTGTGATAAGGTGTTCACAGCG 2135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCTAGATTAGCCCTTGCCTCCATCGGAAAACTCATCTTCGCGCAATTCTCTGAGCTTGTT 1355
CCICTICCTATCTGTTAAGTGTGTTTTTCCAATTGGTTTTCAATTTTTATTTTTATTTTT 2255
                                                                                                                                                                        GTGTGTGATGGAGGGATCATTGATCCATTGTTGGAGTGCCTCAAGAGCTGGGATGGGGCT
                                                                                                                                                                                                                                                             ATCTCCAAAGGTCAAATTATTCATCCGTTGTTGGAGTGTCTTGGAGGGTGGAATGGGGAA 2236
                                                                                                                                                                                                                                                                                                                                                                                                                                               TTTTTGACCGGAGAAAAGGTGACGTCGCGGGAGAGGAGTTCGACAGGGTGTTCACGGCG 2176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATCACCGAGTGCAGGTCTTATCCTCTGTACAAGTTTGTCCGCGAAGAACTCGGGACGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGCACATCAATCTTCCAAAAGATTGCAGCTTTCGAAGACGAACTCAAGGCAGTCCTGCCC 1955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AACACCTCCATCTTCCAAAAGATCGCTACCTTCGAAGAAGAATTGAAAGTCCTGTTACCG 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAGCTCCGACAGGTTCTGGTCGACCACGCTCTAAACAACAGGGGAAAACGGAGAAGAACACT 1936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGCGAATACGTTTTCGCCTACGCCGATGATCCCTGCAGCGCAAACTACCCATTGTTTCAA 1835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGTGAATACGTCTTCGCTTACATCGACGACGTTTGCAGCGGCACATACCCCATTAATGCAG 1876
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTGAAGAACGCAGTGAGGAACACGGTCAACCAGGTGGCCAAGAGGACTCTCACAATGGGC 1715
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAGCTGAGGCAAGTCCTTGTAGATCACGCCCTGCAGAACGGCGAGCACGAGAAGAATGTG 1895
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
                          195 CGGAGGCGTTGACCGGAAGTCACCTTGATGAGGTGAAGAAGATGGTTGCGGAGTTCAGAA 254
                                                                                                                         135 ACGTTAATGGAGTCGTTAATGAGTTGTGCATCAAGGATCCATTGAACTGGGGAGTTGCAG 194
                                                                                                                                                                                                     y Match 50.3%;
Local Similarity 72.1%;
                                                                            99 ACGGGAACGGAATGGATTTCTGCATGAAGACCGAAGATCCGTTGTACTGGGGGAAICGCGG 158
Appert, C., Logemann, E., Hahlbrock, K., Schmid, J. and Amrhein, N. Structural and catalytic properties of the four phenylalanine ammonia-lyase isoenzymes from parsley (Petroselinum crispum N. Eur. J. Blochem. 225 (1), 491-499 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (22-AUG-1994) C. Appert, Institut fuer Pflanzenwissenschaften, Eidgenoessische Technische Hochschule,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Spermatophyta; Magnoliophyta; eudicotyledons; core eudico Asteridae; euasterids II; Apiales; Apiaceae; Petroselinum
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MNKGTDSYGVTGGFARISHRRTKOGGALOKELLRELINAGIFGNASDLVPLSATTAAN
LVRLNTLLGGYTGGFARISHRRTKOGGALOKELLRELITAASGLVENSYIAGLLTAG
RPNSKAVGPTGVILSPEEAFKLAGVEGGFEELQFKEGLALVNGTAVGSGMASMVLFEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="phenylalanine ammonia-lyase
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                                                                                                                                                                                                                                                                                                                                                                                                      LDYGFKGAEIAMASYCSELQFLANPVTNHVQSAFQHNQDVNSI.GLISSRKTSFAVEILKMSTTFLVGLCQAIULRHLEENLKSTVKNTVSSVAKRVLTMGVNGELHPSRFCEKDL
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/EC_number="4.3.1.5"
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0	010 GGATOGAGGANATGOAGGIOTTAGOCATTGTAGAAAGTTTGTGAGGAAAAGKGTTGGGAAATTG	Db
2114	055 GGATTAAAGCTTIGCAGATCGTACCCGTTGTATAGGGTTTGTAAGGGGAGGAGCTCGGCAGAG	Q _Y
2009	750 GEADAGAAGATEGAAAGEGCEGAGAGEGGAAAGEGAAAGEGAAAEGAAA	DB 5
2	890 TGAACACTTCCATCCTTCCAAAAGATTGCGACCTTTGAGGATGAACTAAAGGCCCCTATTGC	da
1994	935 CTAACACCTCCATCTTCCAAAAGATCGCTACCTTCGAAGAAGAAGAATTGAAAGTCCTGTAC	Оy
1889	30 AAAAATTAAGACAAACACTAGTIGAGCATGAGCATGAAGAATGGTGACAACGAGAGAAAAAA	DЬ
1934	875 AGAAGCTCCGACAGGTTCTGGTCGACGACGCTCTAAACAACGGCGAAAACGGAGAAGAACA	Qу
80	770 ACCCCGAATACATTTTTCCATATATTGATGATCCCTGCAGCGCAACCGAACCGACCG	Db
· 20	815 ATCGTGAATAPGTCTTCGCTTACATCGACGACGTTTGCAGCGGCACATACCCATIAATGC	Ûγ
1814 1769	755 GGTICAAGGGGGAGCTICGACCCGTICGAGAFTCTIGTGGGGAGAAGAFTCTGCTGGTGTTAGTTGTTGTTGTTGAGAAGGGTGAGAGATCTCTGTGAGAAGATTTTACTCAGATTTTGTTGT	Db Qy
. 7	650 ATTTAAAAAGCACTGTCAAAAACACAGTAAGCTCAGTAGCTAAGCGAGTACTAACTA	Дb
1754	695 ACATGAAATCGACAGTGAAGAACAGGTAAGCCAAGTCGCGAAAAAAGGTCCTCACCATGG	Qy
1649	590 TGTCTACTACATTTTTAGTAGGCCTCTGCCAAGCAATAGACTTGAGGCATTTGGAGGAGA	Db
1694	635 TGTCGTCGACATACTTAGTCGCTCTATGCCAATCCATCGATTTACGCCATTTGGAAGAGA	Qy
1634 1589	1575 ATTOTOTOGGATTAATTTCAGOGAGGAAAACCGCAGAAGCAGTCGACATCTTAAAACTCA	D Qy
1529	470 ITTTAGCCAATCCAGTGACCAACCATGTTCAAAGTGCTGAACAACACAATCAAGATGTAA	Db
1574	515 TTCTCCCAAATCCAGTCACCAACCATGTTCAAAGCGCGGAACAACACACAC	Qy
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in .	455 IGGACTAODESTICAAAGGTGGAGAAATOGOOATGGTTCTTACTGTTCTGAGCTTCAGT	Α.
1454 1409	CCGGTGGACGTAACCCTAGTT 	40 VQ
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Lithospermum erythrorhizon dedifferentiated cells cell suspension cultures cell_line:M18 cDNA to mRNA, clone_lib:expression_library of Lithospermum cells cultured in pigment production medium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Agriculture, Kyoto University, Lab. Molecular & Cellular Biology,
Div. Applied Life Sciences; Kitashirakawa, Kyoto, Kyoto 606-01,
Japan (E-mail:yazaki@kais.kyoto-u.ac.]p, Tel:075-753-6384,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (16-JAN-1996) Kazufumi Yazaki, Graduate School of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yazaki,K
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                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Ē-mail:yazaki@kais.kyoto-u.ac.jp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  K., Kataoka, M., Honda, G.,
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                                                                                                                                                                                                                                                                                                                     DPLQKPKQDRYALRTSPQWLGPQIEVIRSATKMIEREINSVNDNPLIDVSRNKALHGG
NFQGTPIGVAMDNTRLAIASIGKLLFAQFSELVNDYYNNGLPSNLTGSRNPSLDYGFK
GAEIAMASYCSELQFLANPVTNHVQSAEQHNQDVNSLGLISSRKTSEAVEILKLMSSS
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GVTTGFGATSHRRTKQGGALQKELIRFLNAGIFGNGTETSHTLPHSATRAAMLVRINT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type-"cell suspension cultures"
/clone_lib="expression library of Lithospermum cells
cultured in pigment production medium"
                                                                                                                                                                                                                                                                                                                                                                                                   VGPTGEKINAEEAFRLAGISTGFFELQPKEGLALVNGTAVGSGMASMVLYEANILAVL
SEVISAIFAEVMNGKPEFTDHLTHKLKHHPGQIFAAAIMEHILDGSGYVKAAQKLHEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product-"phenylalanine ammonia-lyase"
/protein_ld-"BAA24928.1"
/protein_ld-"BAA24928.1"
/db_xref="G1:2911122"
/translation="METIVENGNGKTMEFCMKDPLNWEMASESMKGSHLDEVKNMVAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /dev_stage="dedifferentiated cells"
/note="Sieb, et Zucc."
161. .2293
                                                                                                                                                                                                                  FTAMCEGKLVDPLLACLEAWNGAPLPIC"
                                                                                                                                                                                                                                     PKEVENARASVENGIPAISNRIEECRSYPLYKFVREELGTELLTGEKVRSPGEELDKV
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                                                 ATGCCCTCCGTACATCGCCTCAATGGCTTGGTCCTCAGATCGAAGTGATCCGTTCTGCTA
                                                                                                         ATGCTCTCCGTACATCTCCCCAATGGCTCGGACCTCAAATCGAAGTAATCCGATCATCAA 1214
                                                                                                                                                                                                                                                                 ATCCAGGACAGATTGAGGCTGCTGCTATCATGGAGCACATTTTGGATGGTAGTGGATATG
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                                                                                                                                                          TTAAGGCTGCTCAGAAGTTACATGAGATGGATCCTCTGCAGAAGCCTAAGCAAGATCGTT
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search completed: March 28, 2003, 23:39:52 Job time : 6255 secs

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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result		Query				
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EST495692	HG5K10.7	EST509260	51-38 Ste	27006	OCC6M01.y	QGG361.13.	HB34C14.	EST301314	ST553180	@GG10L14.	EST594791	EST431938	OHH9H1 - 7	50TE	QHF7N21.y	QHH15012.	EST580829	EST513848	EST506886	QHG3h02.y	103G09 Ma	OHC12F14.	HH1cl0.7	OHH12A03.	ST-46323	QHH2105.y	QHH6L12.y	EST506883	OCCEPANDE.	OHF4c07.y	QGH13K13	QGC5F22.y	QGG27H21.	OGH4h01.y	ось7F21.у	QGG1 8H05.		QGD5H12.y

ALIGNMENTS

אסתו כפ אסתו	FEATURES	JOURNAL	TITLE	AUTHORS	JOURNAL	TITLE	AUTHURS	REFERENCE		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	POCAS	RESULT 1 AY103647
/organism="Zea mays" /db_xref="MaizeDH:638378" /db_xref="taxon:4577" /cloue="FCG142084"	Location/Qualifiers	Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA	Direct Submission	2 (bases 1 to 2598) Coe, E.C.	Unpublished (2002)	Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes	Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.	1 (bases 1 to 2598)	bukaryota, Virtaipiantae, Streptopnyta; Embryopnyta; fracheopnyta; Spermatophyta; Magnoliophyta; Liliopsida; Puales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.	Zea mays	Zea mays.	HTC.	AY103647 1 G1:21206725	Zea mays PCol42084 mRNA sequence. AY103647	AY103647 2598 bp mrNA linear HTC 25-MAY-2002	

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ORIGIN
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1010 САСТТВАСАСАВААТТВААВСАТСАСССТВЭТВАААТВВАВНЭЭЭЭЭЭЭЭЭТЭАТГАТВВАН 1059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     470 AAGCAAGGCGGTGCTTTACAGAAGGAGCTCATTAGATTTTTGAACGCCGGAATATTCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             140 GACCCGCTGAACTGGGGCGGCGGCGGCGGAGCTGGCCGAGCCACCTGGACGAGGTG 199
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                                                                                    TOGGAGGTOCTGTCCGCCGTCTTCTGCCGAGGTCATGAACGGCAAGCCCGGGGTACACGGAC 976
                                                                                                                                                                 TCGGAAGTGTTATCGGCGATCTTCGCTGAGGTTATGCAAGGGAAGCCGGAGTTTACCGAT 1009
                                                                                                                                                                                                                                                                                                                  GCCGTGGGGTCCGGGATGGCTTCCATGGTTCTATTTGATGCTAATGTACTTGCGTTGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTTGAAGGTGGGTTCTTCGAGTTACAGCCGAAAGAAGGGGCTAGCACTTGTTAACGGCACC 889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAGGCCGTCACCGTCGACGGGAGGAAGGTGGACGCCCGACGCGTTCAAGATCGCCGGC 796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAAGCCGTTGGCCCCACCGGAGAAGTCCTCAATGCCGAAAAGGCCTTCGCTGCAGCGGGA 829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCCGGTGACCTTGTCCCATTATCATACATCGCCGGCCTCTTAACCGGCCCCCAACTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCGGCAGCGA----CGGGCACACGCTGCCGTCGGAGGTCACCCGCGGCGATGCTGGTG
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                                                                                                                                                                                                                                             TCCGTGGGCTCCGCGCCGCCACCGTGATGTACGACGCCAACGTCCTGGCCGTCCTG
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Library"
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                                                                                                                                                                                                158
                                                                                                                             494
                                                                                                                                                                                                                             434 ACCACCGCCTTCCGCCCCCCCCCCCCCGCAGACTAAGCCAAGGCGGTGCTTTACAGAAG 493
335 TACTCCGGCATATOGGCTTCGAGGATOCTOGAGGGCATCATOAGGTCATOAGGATCATOAGGTC
                                614 TACTCCGGCATCCGATTCGAGATCTTGGAAGCCATCACCAAGTTCCTTAACAACAACATC 673
                                                                                374 ΑΛΘΑΘΑΛΙΤΑΘΤΑΘΤΑΘΕΠΑΤΟΘΑΝΙΑΘΑΛΑΘΑΝΑΛΑΓΑΛΑΓΑΛΑΘΑΑΝΑΝΤΟΙΛΤΑΘΕΤΑΤΘΕΤΘΤΟ 433
                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                              98 ATGGCGAGCAACACGCCATCCTGGACTGCATCGCCACGGCGGCGACACCTACGGCGTC 157
                                                                                                                                                              GAGCTCATTAGATTTTTGAACGCCGGAATATTCGGCAATGGAACGGAAACAAGCCACACA 553
                                                                 CTCCCGTCCGAGGTTTCGCGTGCGGGCCATGCTCGTCCGCATCAACACCCTCCTCCAGGGC
                                                                                                                                                                                            Coe,
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Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
Maize Mapping Project/DuPont Consensus Sequences for Design of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae; PACC Clade, Panicoldeae, Andropogoneae, Zea.
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Zea mays
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                                                                                                                                                                                                                                                                  Department of Vegetable Crops, R.W.Michelmore Lab University of California at Davis (UCD) Asmundson Hall, UCD, Davis, CA 95616, USA
                                                                                                                                                                                                                                                                                                                                                                              http://compgenomics.ucdavis.edu/
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegle,J., Elli,P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y., Lai,Z., Church,S., Jackson,L. and Bradford,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta, Embryophyta, Tracheophyta, Spermatophyta; Magnoliophyta, eudicotyledons, core eudicots; Asteridae; euasterids II; Asterales; Asteraceae; Lactuceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BQ850732 759 bp mRNA linear bsi 14-AUG-2000. QGB13G17.yg.abl QG_ABCDI lettuce salinas Lactuca sativa cDNA clone
                                                                                                                                                            Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu] belongs to contig QG_CA_Contig6760, see http://cgpdb.uc
                                                                                                                                                                                                                                                                                                                                                       Contact: Alexander Kozik [R.W.Michelmore]
                                                                                                                                                                                                                                                                                                                                                                                                                                   Church,S., Jackson,L. and Bradford,K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L
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/organism="Lactuca sativa"
/cultivar="Salinas"
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                              1549 CGCCGAACACACACTCAAGACGTTAATTCTCTCGGATT 1587
                                                                                                                   1429 TCTCTCCGGTGGACGTAACCCTAGTTTGGACTACGGGTTCAAAGGTGGAGAAATCGCCAT 1488
                                                                                                                                                                                                                                                                                                                                                                               1369 CATGTTCGCTCAATTTTCTGAGCTGGTTAACGATTTCTACAACAATGGATTACCATCGAA 1428
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                                                                                        541 CATGTTCGCTCAATTTTCTGAGCTGGTTAACGATTCTACAACAATGGATTACCATCGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         421 CGACAACCCATTGATCGACGTTTCCAGAAACAAAGCTTTACACGGTGGTAACTTCCAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             361
                                                                                                                                                                                                                                                                                                                                                                                                                                         481 ANCCCCAATCGGAGTTTCCATGGACAACACCCGTCTCGCCATTGCTGCAATCGGAAAACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 TCACTTGACACACAAATTGAAGCATCACCCTGGTCAAATCGAGGCGGCGGCGGCGATCATGGA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 GTCGGAAGTGTTATCGGCGATCTTCGCTGAGGTTATGCAAGGGAAGCCGGAGTTTACCGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   829 AGTTGAAGGTGGGTTCTTCGAGTTACAGCCGAAAGAAGGGCTAGCACTTGTTAACGGCAC 888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 CGCCGTGGGGTCCGGGATGGCTTCCATGGTTCTATTTGATGCTAATGTACTTGCGTTGTT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCAAATCGAAGTAATCCCATCATCAACCAAAATGATCGAGAGGGAAATCAATTCCGTCAA
                                                                                                                                                                                                     TCTCTCCGGTGGACGTAACCCTAGTTTGGACTACGGGTTCAAAGGTGGAGAAATCGCCAT
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TAG_LLB=QG_ABCD1 lettuce salinas
TAG_TISSUE-chem.cal induction
TAG_SEQ=TGTAGCCGGG"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transformations made with four size classes to minimize
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/clone="QGB13G17"
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721 CCCCGAACACACACICAAGACGTTAATTCTCTCGGATT 759

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                    1044 AAATCCAGGCGGCGGCGATCATGGAGTATATTTTGGACGGAAGCGATTACGTCAAGGCGG 1103
                                                                                                                                                             864 AAGGGCTAGCACTTGTTAACGGCACCGCGGTGGGGTCCGGGGATGGGTTCCATGGTTCTAT 923
                                                                                                                                                                                                                                                                                              301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             684 TACCCCTCCGTGGAACCATCACCGCCTCCGGTGACCTTGTCCCCATTATCATACATCGCCG 743
                                                                                                                                                                                                                                                                                                                                     804 CCGAAAAGGCCTTTCGCTGCAGCCGGAGTTTGAAGGTGGGTTTCTTCGAGTTTACAGCCGAAAG 863
                                                                                                                                                                                                                                                                                                                                                                                                              744 СОСТСТТАЛОССКИ СЕССОЛЛОТЕССАЛЛЕН СЕТТЕНО СОССАСОВНАВЛЕНОСТОЛАТЕ 803
                                                                                                                                                                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Y Match 31.0%;
Local Similarity 68.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TGCCGCTCCGGGGCACCATCACCGCGTCGGGGGGACCTCGTCCCGCTCTCATACATCGCCG 60
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                                                                                                                                                                                                                     AGGGCCTCGCCATGGTCAACGGCACCGTGGGGTTGGGGCTTGGGGCTGCACCGTGCTCT 240
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Hainey, C.F., Dolan, M., Mido, G. H., Vogel, T.M., Whitsitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V. Maize Mapping Project/DuPont Consensus Sequences for Design overgo Probes
Overgo Probes
Open (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (25-APR:2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA
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Spermatophyta, Magnoliophyta, Liliopsida; Poales, Poaceae; PACC
clade, Panicoldeae, Androposturae, 25a
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1943 TOCATCTTOCAAAGATOGOTACCTTCGAAGAAGAATTGAAAGTOCTGTTACCGAAAGAA 2002	DP AA
1883 CGACAGGETCIEGE ICGARCACGETETIAAACAACGCCGAAACGGAGAAGAACACTIAACACC 1942	Су
1823 IACSTOTTOSOTTANATOSANGANSTITES/ASSESSANATANANONATIANTONASANSSIC 1882	dd 67
1763 GERGAGATOMARCOSTOGAGATICTIGNIGAGAAGATETPOTEOGIGITIGATIGATOSTGAA 1822 	DP VQ
1703 TGGACAGTGAAGACACCGTAAGCCAAGTGGGGAAAAAGGTCCTCAACATGGGGCTCAAC 1762 1 1 1 1 1 1 1 1 1	ДУ
1643 MATACETANEGGETCTATESCCANECCATEGACTATAGGECATITEGAAGAGAACATGAAA 1/02	d Vy
1583 GGATTAATTT AGGGAGGAAAAN GGAGAAAA TARTGAAATTTAAAACTGATGGGGGGAGAGGGGAGAAAACTGATGGGGGGAGAAACGGGGGGGAGGGA	47 79
1523 AATCCAGTCAGCAACCATGTTCAAAAGCGCGGAACAAACA	έş.
1463 GAGITCANAGGIGGAGANAAA (GGCTTCITA) TAJITCIGAGCITCAGTITCIGCO 1522 	ής γγ
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128 GETTTANACESTGGTANITECCANSIAN COCATOGGGITTCCATGGACANACACCCST	
1223 ATCGARGAGAAATCAATTCCSTCAACGACAACCAATGATCGACGACGACGATAAACAAA 1282 	방
1163 GGTAGA FGTGGGGAATGGGTGAGAGCFGAAA FGGAAGTAAATGGGATGATGAGGAAGGAAAATG 1222 	Ę Qy
1104 GACAAAAASTICCACSA AATASA CCGTTACASAAACCAAAACAAAAACATCGTIATGCTCTC 1162	Qy
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QGF21N06.yg.abl QG_EFGHJ lettuce serriola Lactuca sativa cDNA clone
QGF21N06, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
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Lettuce and Sunflower ESTs from the Compositae Genome Project
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Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegle,J., Ellis
,P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y., Lai,Z.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Alexander Kozik [R.W.Michelmore]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae, Streptophyta, Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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                                                                                                                                                                                            TAG_LIB=QG_EFGHJ lettuce serriola
TAG_TISSUE=leaves dark grow
TAG_SEQ=GCTAGTCGGG"
                                                                                                                                                                                                                                                   transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at http://capdb.ucdavis.edu/
                                                                                                                                                                                                                                                                                                            source of RNA. eDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and
                                                                                                                                                                                                                                                                                                                                               /note-"Vector: pBRcDNASIIAB; The library was constructed from 10 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each
                                                                                                                                                                                                                                                                                                                                                                                                                                  /lab_host="E.coli"
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                                                                                                                                                                       Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L., Lin,H., van Damme,M., Lavelle,D., Chevaller,P., Ziegle,J., Elliss,P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y., Lai,?., Church,S., Jackson,L. and Bradford,K.

Lettuce and Sunflower ESTs from the Compositae Genome Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids II; Asterales; Asteraceae; Lactuceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UNH9N08.yq.abl QG_EFGHJ lettuce serriola Lactuca sativa cDNA clone OGH9N08, mRNA sequence.
Department of Vegetable Crops, R.W.Michelmore Lab
                                              Contact: Alexander Kozik [R.W.Michelmore]
                                                                                                                                       http://compgenomics.ucdavis.edu/
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579 CTAATGTACTTGCGTTGTCGGAAAGGTTATCGGCGATCTTCGCTGAGGTTATGCAAG 638
                                                        930 CTAATGTACTTOGGTTTGTTGGGAAGTGTTATTGGGGGATGTTTGGGTGAGGTTATTGCAAG 989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOOSTGGAACCATCACCGCCCCGGAGGAGCCTGTCCCCATTATCATACAGCGCGGCCTCT 749
                                                                                                                       TAGGACTTGITAA GASA GCGAGGTGGGGGGGGGGGGGGGGGGGGTGGTTGGATG
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                                                                                                                                                                                                                                                                                                                            AGRICUTTURA TURAR CONSACTIGAN RETRESTECTION ACTITACA ROUGANA CANAGRAGIC 869
                                                                                                                                                                                                                                                                                                                                                                                               TAACCGGCCGCCCAA: TCCAAAGGCGTTGGCCCACCGGAGAAGTCCTCAATGCCGAAA 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TAACCGGCCCCCAACTCCAAAGCCCTTTGGCCCAACGGGAGAGTCCTCAATGCCGAAA 809
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                                                                                                                                                                                                                                                            AGGCCTTCGCTGCAGCCGGAGTTGAAGGTGGGTTCTTCGAGTTACAGCCGAAACAAGGGC 518
                                                                                                                                                                                                                                                                                                                                                                                                                                  for details.

Plate: QGH9 row: N column: 08.
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Asmundson Hall, UCD, Davis, CA 95615, USA
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belongs to contiq QG_CA_Contig6760, see http://cgpdb.ucdavis.edu/
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Fax: 1-(530) -752-9659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  188 a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAG_SEQ-Not found"
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/db_xrei-"taxon:4236"
/clone-"QGH9NO8"
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/lab_host="E.coli"
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98.8%;
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-830 - GTTGAAGGTGGGTTCTTCGAGTTACAGGCGAAAGAAGGCTAGCACTTGTTAACGGCACC-889

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Score 694.4; DH 1 Pred. No. 6.7e:82; Mismatches

DH 14; Length 710;

Best Local Similarity

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QGD5H12.yg.abl QG_AHCDI lettuce salinas Lactuca sativa cDNA clone

QGD5H12, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2002)
Contact: Alexander Kozik [R.W.Michelmore]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Church, S., \  \  Jackson, L. \  \  and \  \  Bradford, K. Lettuce and Sunflower ESTs from the Compositae Genome Project
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Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegle,J., Ellison
,P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y., Lai,Z.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for details.
Plate: QGD5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu] belongs to contig QG_CA_Contig6760, see http://cgpdb.ucdavis.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Asmundson Hall, UCD, Davis, CA 95616, USA Tcl: 1-(530)-742 1742 Fax: 1-(530)-752-9659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         University of California at Davis (UCD)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://compgenomics.ucdavis.edu/
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                                                                                                                                construction can be obtained at http://cgpdb.scdavis.edu/
TAG_LIB-QG_ABCDI lettuce salinas
TAG_TISSUB-chemical induction
                                                                                                                                                                                                                size bias. Details of each source of RNA and library
                                                                                                                                                                                                                                      source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize
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/clone="QGD5H12"
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                                                                                                                                                      Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L.,
Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegle,J., Ellison,P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y., Lai,Z.,
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EST.
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Department of Vegetable Crops, R.W.Michelmore Lab University of California at Davis (UCD)
                                           Contact: Alexander Kozik [R.W.Michelmore
                                                                      Unpublished (2002)
                                                                                          http://compgenomics.ucdavis.edu/
                                                                                                                  Church, S., Jackson, L. and Bradford, K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
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                                           1370 ATGTTCGC1CAATTTCTGAGCTGGFFAACGATTCTACAACAATAGGATTACCATCGAAT 1429
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belongs to contig OG_CA_Contig6760, see http://cgpdb.ucdavis.edu/
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TAG_LIB-QG_ABCDI lettuce salinas
TAG_TISSUB-chemical induction
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/cultivar="Salinas"
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Cepartment of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
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Lettuce and Sunflower ESTs from the Compositae Genome Project http://compgenomics.ucdavis.edu/
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P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y., Lai,Z.,
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EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
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1-(530)-752-9659
                                                                                                                                                                                                                                                                      construction can be obtained at http://cgpdb.ucdavis.edu/
TAG_LIB-QG_EFGHJ lettuce serriola
TAG_TISSUF-leaves dark grow
                                                                                                                                                                                                                                                                                                                                                                                                 Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of kNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and
                                                                                                                                                                                                                                                                                                                                                  transformations made with four size classes to minimize size bias. Details of each source of RNA and library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note-"Vector, pBRcDNAS(IAB; The library was constructed from 10 different sources of RNA from a single genotype.
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unpublished (2002)
Contact: Alexander Kozik [R W Michelmore]
Contact: Alexander Kozik [R W Michelmore]
Department of Vegetable Crops, R W Michelmore
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
                                                                                                                                                                Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L.,
Lin,H., van Damme,M., Lavelle,D., Chevaller,P., Ziegle,J., Ellison,P., Kolkman,T., Slabaugh,M.S., Livingston,K., Zhou,Y., Lai,Z., Church,S., Jackson,L. and Bradford,K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
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601 GCTAGCACTFOFFAACGGCACCGCCGTGGGGTCCGGGATGGCTTCCATGGTTCTATT 657

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ORIGIN
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                                                                                                                                                                          AAAGGCCTTCGCTGCAGCCGGAGTTGAAGGTGGGTTCTTCGAGTTACAGCCGAAAGAAGG 867
                                                                                                                                                                                                                                                      CTTAACCGGCCGCCCCAACTCCAAAGCCGTTGGCCCCACCGGAGAAGTCCTCAATGCCGA 540
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for details.
Plate: QGD7
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                                                                                                          ACACAATTAGATTGTTCTTGTTTCTTTGATCTATAGTCTACAATCTGTATAAACAATAAT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Department of Vegetable Crops, R.W.Michelmore University of California at Davis (UCD) Asmundson Hall, UCD, Davis, CA 95616, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Alexander Kozik [R.W.Michelmore]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 6/9)

Kozik,A., Michelmore,P.W., Knapp,S., Marvionko,M., Rieseberg,L.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyjedons; core eudicots; Asteridae; euasterids II; Asterales, Asteraceae, Lactuceae;
                                                                                                                                                 University of California at Davis (JCD) Asmundson Hall, UCD, Davis, CA 95616, UTel: 1-(530)-742 1742
Fax: 1-(530)-752-9659
                                                                                                                                                                                                                                                      Contact: Alexander Kozik [R.W.Michelmore
                                                                                                                                                                                                                                                                                 Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST.
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                                                                                                                                                                                                                                    Department of Vegetable Crops, R.W.Michelmore Lab
                                                                                                                                                                                                                                                                                                 http://compgenomics.ucdavis.edu/
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Lettuce and Sunflower ESTs from the Compositae Genome Project
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                                                              Plate: QGG27 row. H column: 21.
                                                                                     for details.
                                                                                                       belongs to contig QG_CA_Contig6760, see http://cgpdb.ucdavis.edu/
                                                                                                                         Email: akozik@atgc.org {michelmore@vegmail.ucdavis.edu}
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lactuca
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Best Local Similarity 96.9%;
                                                                                                                                             1360 CGGANAACTCATGTTCGCTCANTTTTCTGAGCTGGTTAACGATTTCTACAACAATGGATT 1419
                                                                                                                                                                                                                                          1300 CHICCAAGGAACCCCAAFCGGAGFFFGCAFGGACAACACCCGFCTCGCCAFTGCTGCAAF 1359
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ACCATCGATCTCCCGGTGGACGTAACCCTAGTTTGGACTACGGGTTCAAAGGT 1474
                                                                                                                                                                                             CTTCTAAGGAACOJCAATOJGAGTTTCCATGGACAACACOGGTCTCGCCATTGCTGCCGCCAT 540
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/clone_lib-"QG_EFGHJ lettuce serriola"
/lab_host-"E.coli"
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242 GGTTACTCCGGCATCCGATTCGAGATCTTGGAGGCGATCACCAAGTTCCTCAACCACAAC 301
                                                                                                                                                                                                                                                                                                                                                                                                          431 GTCACCACCGGCTTCGGCGCCACCTCTCACCGGAGAACTAAGCAAGGCGGTGCTTTACAG 490
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                                                                                                                                                                                                                                    122 AAGGAGCTCATTAGATTCTTGAACGCCGGAATATTCGGTAATGGCACAGAATCAACCCAC 181
                                                                                                                                                                                                                                                                                                                                                       62 GTCACTACCGGGTTCGGAGCTACCCCTCACCGGAGAACGAAAGAAGGTGGTGCTCTTCAG 121
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                                                            GGTTACTCCGGCATCCGATTCGAGATCTTGGAAGCCATCACCAAGTTCCTTAACAACAAC 670
                                                                                                                        ACACTTCCACATTCAGCCACAAGAGCAGCCATGCTTGTCAGAATCAACACCCTCCTTCAA 241
                                                                                                                                                ACACTTCCACACTCAGCCACCAGAGCCGCCATGATCGTCAGAATCAACACCCCCCCTCCAG 610
                                                                                                                                                                                                                                                                                          AAGGAGCTCATTAGATTTTTGAACGCCGGAATATTCGGCAATGGAACGCAAACAAGCCAC 550
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University of California at Davis (UCD)
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/db_xref="taxon:4236"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Department of Vegetable Crops, R.W.Michelmore University of California at Davis (UCD) Asmundson Hall, UCD, Davis, CA 95616, USA
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                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
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/note-"Vector: pBRcDNAS(iAB): The library was constructed from 10 different sources of RNA from a single genotype. Separate coNAS were generated using primers that incorporated unique 5' and 3' tags to distinguish each
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                                                                                                                                                                                                                                                                                                                                                              AGCCTTCAATTTCGGAGGAGTTACTTGGTGGGCTCTTTGAGCTACAACCTAAAGAAGGTCT 669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CACCTCTCACCGGAGGACCAAGCAAGGGGGTGCTCTTCAGAAGGAGCTCATTAGATTTCTT 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CACTGTGAAGGTGGAGCTGTCGGAGACTGCTATGGCTGGAGTGAAAGCGAGTAGTGATTG
                                                                                                           OHF4e07.yg.abl QH_EFGHJ sunflower RHA280 Helianthus annuus cDNA clone QHF4e07, mkNA sequence.
Helianthus annuus
Eukaryota; Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
                                                                      EST.
                                                  common sunflower.
                                                                                         BU024517.1 GI:22460037
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source of RNA. CDNAS were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size blas. Details of each source of RNA and library construction can be obtained at http://cgpdb.ucdavis.edu/
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                                                                                                                                                                                                                                                                                                                                                                                                  881 AACGGCACCGCGTGGGGTCCCGGGATGGCTTCCATGGTTCTATTTGATGCTAATGTACTT 940
                                                         301 CANGCIGGCGIAGAAGGCGGAITCITCGAGTIAGAGCCAMAGAAGGCICCCTCGCGCTIGIT
                                                                                                                  821 GCAGCCGGACTTGAAGGTGGGTTCTTCGAGTTACAGCCGAAAGAAGGGCTAGCACTTGTT 880
                                                                                                                                                                            241
                                                                                                                                                                                                                         761 CCCANTECAMACCOTTIGGECEACGGIAGANID CTCAATGECGAAAGGCCTTCGCT 820
                                                                                                                                                                                                                                                                                                                                               701 ATCACCGCCTCCGGTGACCTTGTCCCATTATCATACATCGCCGGCCTCTTAAGCGGCCGC 760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               581 ATGATESTCAGAATCAACACCTCCTECAGGGTTACTCCGGCATCCGATTCGAGATCTTG 640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            521 ATATTCGGCAATGGAACGGAAACAAGCCACACACTTCCACATTCAGCCACCACAGCCGCC 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 ATGTTGGTCAGAATCAACACCCTCCTCCAGGGATAFTCCGGCCATAAGATTCGAAATCTTG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | CCCAACTCAAAGGCAGTTGGCCCGGGCGGTGAAGTTCTCAATGCGGAATCCGCATTCGCC
                                                                                                                                                                                                                                                                                      ATCACCGCCTCCGGTGACCTCGTCCCGTTGTCCTACATCGCGGGGTCTCCTCACCGGCCGA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        588; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 696)

Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L.,
Lin,H., van Damme,M., Lavelle,D., Chevaiier,P., Ziegle,J., Ellis
,P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y., Lai,Z.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Church,S., Jackson,L. and Bradford,K.

Lettuce and Sunflower ESTs from the Compositae Genome Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 84 6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for details.
Plate: QHF4 row: e column: 07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email. akozik@atye.org {michelmore@vegmail.ucdavis.edu} belongs to contig QH_CA_Contig3142, see http://cgpdb.uc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Department of Vegetable Crops, R.W.Michelmore Lab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Alexander Kozik [R.W.Michelmore]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Spermatophyta; Magnoliophyta, eudicotyledons, core eudicots;
Asteridae; euasterids II; Asterales; Asteraceae; Asteroideae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               size bias. Details of each source of RNA and library construction can be obtained at http://cgpdb.ucdavis.edu/
TAG_LIB=QH_EFGHJ sunflower_RHA280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TAG_TISSUE*chemical induction TAG_SEQ*TGTAGCCGGG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Separate CDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:4232"
/clone="QHF4e07"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note=""Vector: pBReDNASfiAB; The library was constructed from 11 different sources of ENA from a single genotype.
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/lab_host="E.coli"
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- Оy Бþ Ş γQ Qy dcl Qy Дb Ъ Вρ Вb 1121 ATGGACCCGTTACAGAAACCAAAACAAGATCGTTATGCTCTCCCGTACATCTCCCCCAATGG 1180 1001 TTTACCGATCACTTGACACACAAATTGAAGCATCACCTGGT'AAAT''AAAT''AAGG'AGGCAGCC 1050 601 ATGGACCOGTTACAAAAACCAAAAACAAGACGTTACGAGGCTCAGGAGGTCACGTCAATGG 650 361 AATGGTACCGCGGTGGGGTCCGGGGTCCATGGTCTTGTTTGAAGCCAATGTACTT 420
- Search completed: March 29, 2003, 00:34:00 Job time : 3134 secs

Genuore version 5.1.4_p5_4578

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Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Database .
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Listing first 45 summaries
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                                                                                                                              /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.scq:*
/cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
                                                                                                                                                                                                                                                        /cgn2_6/ptodata/1/pubpna/USUb_NEW_PUB.Scq:*
/cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.scq:*
/cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.scq:*
/cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.scq:*
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/cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
                                                                                                                                                                                             /cgn2_6/pt.odata/1/pubpna/US08_NEW_PUB.seq:*
/cgn2_6/pt.odata/1/pubpna/US08_PUBCOMB.seq:*
/cyn2_6/ptudata/1/pubpna/US10_NEM_PUB.seq:*
/cyn2_6/ptudata/1/pubpna/US10_NEM_PUB.seq:*
/cyn2_6/ptudata/1/pubpna/US60_NEM_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query Match Length DB	BH	Œ	Description
1	2442	100.0	2442	9	US-09-964-992A-3	Sequence 3, Appli
C4	1603 B	65.7	2380	د	IIS - 09 - 964 - 992A - 4	4
ىپ	1208.8	49.5	2154	9	US-09-938-842A-813	813
4	1203.2	49.3	2178	9	US-09 938-842A-1713	Sequence 1713, Ap
IJī	549.6	:1 :2 :5	912	10	US · U9 · 854 · 122 · 46	Sequence 46, Appl
ი ი	270.6	11.1	660	10	115-09-770-149-476	
7	265.6	10.9	2163	10	US-09-939-408A-29	Sequence 29, Appl
ထ	256	10 5	2475	10	IIS-09-939-408A-20	20,
4	244	10.0	2419	10	US-09-939-408A-12	-
10	877	٠ ب	2747	=	US-09-939-408A-16	16,
11	223.4	9.1	2061	10	US-09-765-873A 31	31,
12	223 4	د 1	2151	10	US-09-765-873A 7	7,
13	221.8	9.1	2439	10	US-09-939-408A-18	18,
14	220.2	9.0	2151	10	US · 09 · 765 · 873A · 9	
15	198.8	8.1	363	10	US-09-878-574-3252	Sequence 3252, Ap
16	171.4	7.0	278	10	US · 09 · 878 · 574 · 10900	Sequence 10900, A
17	169.6	6.9	335	2	US-U9-878-574 2410	Sequence 2410, Ap
18	155.6	5 4	2311	10	US-09-939-408A-14	
19	126	.z	279	10	US-09-878-574-7623	

66, Appl	Sequence	US-09-739-254-66	10	554	2	S.S.	4.5	
11234, A	Sequence	US-09-960-352-11234	10	419	د ۽ سا	55	44	
9335, Ap	Sedifetice	05-09-960-452-9335	10	380	K.	55.4	4 4	
4584, A	Sequence	US-09-960-352-4584	10	416	2.3	55.8	42	
8414, A	Sequence	US-09-960-352-8414	10	312	2.3	55.8	41	C
7419, Ap	Sequence	US-09-960-352 7419	10	377	2.3	56	40	O
12673, A	outlettbes	US-09-960-352-12673	10	277	2 3	56.4	39	
11930,	Sequence	08-09-960-352-11930	1=	Rose	1.	15 E	â	3
11699,	authanthas	ITS-04-460-452-11644	10	215	ر. س	56.8	٦7	2
6783, Ap	Sequence	US-09-878-574-6783	ij	25 ņ	2.4	58.8	<u>ن</u> 1	
4838, A	Sequence	US-U9-294-093B-4838	10	300	2.5	6U	35	
15014, A	Sequence	US-09-960-352 15014	10	375		60.2	34	
11218, A	Soditonos	IIS-09-960-352-11218	10	424	ر ا ار	61	ند	7
7987, A	Sequence	US-09-815-242-7987	10	1530		61.8	ند. د ۱	
9335, A	Sequence	US 09 980 352 9335	10	0.85		Œ.	<u>\$1</u>	n
12673, A	Sequence	US-09-960-352-12673	10	277	2.6	63	30	C
579, Ap	Sequence	US-114-77U-696-579	j	146	2.7	ታን ተ	29	3
8806, A	Sequence	US-09-878-574-8806	10	267	3.4	82.2	28	
7670, Ap	Sequence	HS-H9-878-574-7670	=	i s	٠. ښ	95 Z	27	
1690, Ap	eottetibes	IIS-49-924-876-1690	Į.	5.53	og.	65 L	 	
627, Ap	eddet.bes	IIS-09-770-696-627	٥.	130	-	85 12	r)	
6120, A		US-U9-878-574-6120	C	1 u 5	3.6	87.4	ر ا ح	
3186, Ap	Sequence	US-09-923-876-3186	10	281	3.9	94.2	ιs	
7496, A	Sequence	US-U9-878-574-7496	c	387	ω ω	94. B	t.	
. 28, Appl	eullet.bes	75-04-444-40KA-28	Ξ	2741	4 1	100.2	1.	
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NAME/KEY: CDS
; LOCATION: (119) (2254)
; OTHER INFORMATION: PAL1
US-09-964-992A-3
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; Patent No. uS20020173633A1
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                                                                                                                                              Query Match 100.0%, Score 2442,
Best Local Similarity 100.0%, Pred. No. 0;
Matches 2442; Conservative 0; Mismatches
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APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Characterization of Phenylalanine Ammonia-Lyase (PAL)
TITLE OF INVENTION: Gene in Wounded Lettuce Tissue
FILE REFERENCE: 023070-124500US
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APPLICANT: Campos, Reinaldo
APPLICANT: No. US20020173633Alogaki, Hiroyuki
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                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: lettuce phenylalanine ammonia-lyase (PAL) 1 OTHER INFORMATION: (LSPALL) cDNA
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TYPE: DNA
Mismatches
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APPLICANT: Campos, Reinaldo
APPLICANT: No. US20020173633Alogaki, Hiroyuki
APPLICANT: Suslow, Trovor
APPLICANT: The Regents of the University of Ca
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LOCATION: (77)...(2218)
OTHER INFORMATION: PAL2
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Similarity 85.5%;
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                                        SEQ ID NO 813
LENGTH: 2154
                                                                                        APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSCENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
TITLE OF INVENTION: SAME, AND METHODS OF USE
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2000-08-24
PRIOR FILING DATE: 2000-08-24
PRIOR FILING DATE: 2000-01-16
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-06-22
NUMBER OF SECULIA NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SECULIA NUMBER: US 60/300,111
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                                                                            NUMBER OF SEQ ID NOS: 5379
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ORGANISM: Arabidopsis thaliana
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                                                             TIGGAAAGGTGAAATTATTGATGCGTTGGTTGGAGTGTCTTGGAGGGTGGAATGGGGAACCT 2239
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SEQ ID NO 1713
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APPLICANT: Kreps, Joel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Wang, Xun APPLICANT: Zhu, Tong
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OPGANISM: Arabidopsis thaliana
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708 COLOGGEGACOTEGECCIATIATOATACATOGOGGCOGCIANOCIGGCGCCCANCE 767
                                                                                                                                                             512 IACGAATCAACACTCTCCTCCAACGATTTTTCCGGTATCCGATTTGAGATTCTCGAAGAACSAA 571
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                                                     TTACCAGTTTCCTCAACAACAACATCACTCCATCTCTCCCCCTCCGTGGTACAATCACCG
                                                                                                             TICACCAAGTTTCCTTTAACAACAACAACATCACCCCTTGCTTTTACCCCCTTCGGTTGGAACCATTCACCG 707
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                            1788 GCGAGAAAGATCTCCTCCGTGTTGTTGATCGTGAATACGTCTTCGCTTACATCGACGACGACG
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                                                                                   1652 AAGTGGCGAAGAAGTTCTTACTACTGGAGTCAATGGTGAGCTTCATCCTTCTCGCTTCT
                                                                                                                                       1728 AAGTCGCGAAAAAGGTCCTCACCATGGGCGTCAACGGCGAGCTCCACCCGTCGAGATCCT 1787
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APPLICANT: ALBERTE, RANDALL S.
APPLICANT: SMITH, ROBERT
TITLE OF INVENTION: TRANSGENIC PLANTS INCORPORATING TRAIT OF ZOSTEPA MARINA
FILE REFERENCE: PHA-007.01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 46
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                                                                                                                                                                                                                                                                                                                                                                                                           Matches 672;
                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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CURRENT FILING DATE: 2001-09-10
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PRIOR FILING DATE: 2000-05-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH. 912
TYPE: DNA
ORGANISM: Zostera marına
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                            1312 COCAATOSGAGTTTOCATSGACAACACOCGTOTOGOCATTGCTGCAATOGGAAACCCAT 1371
                                                                                                                                                                                                                                                                                                                       1132 ACAGAAAACGAAACAAGAAGATGTTATGCTCTCCGTACATGTCCCCAATGGCTCGGTAACCTCA 1191
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                                                                                                          1252 MARCHMATTGATGAMGTTTDONGANAGANAGCTTTAGAGGGTGGTARGTTDONAGGAAC 131:
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                                                                                 157 CAACCCACTCATCGATGTCTCCCGTAACAAGGCTCTCCACGGCGGAAACTTCCAAGGCAC 216
                                                                                                                                                                                                                                                                                                   37 AAAGAAGTCGAAACAGGACAGGTACGCTCTTCGGAACGTCTCCCCAGTGGCTGGGTTCCCCA
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                                                                                                                                                                                         GGTGGAAGTTATTUGAGUATUGACCAAGTCGATAGAGUGAGAGATCAACTUUGTGAATGA 156
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                    TITLE OF INVENTION:
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  OF INVENTION:
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                                                                                                                                                                                                                                                                                                                       Raines,
Yu, Yang
                                        Hurban, Patrick
                                                                                                                                                                                                                               Page, Amy
Matthew, Abraham V
Ledford, Brooke L.
                                                            Hoffman, Neil
                                                                               Davis, Keith R. Allen, Keith
                                                                                                                     Kricker, Maja
Slader, Ted
                                                                                                                                                                       Garcia, Carlos A.
                                                                                                                                                                                         Woessner, Jeffrey P
Haas, William David
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                                                                                                                                                                                                                                                                                                                                                                Price, Jennifer L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : Sequence 29, Application US/09939408A ; Patent No. USZUÜZULUZ712A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                       ; GENERAL INFORMATION:
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                                                                               CURRENT APPLICATION NUMBER: US/09/939,408A
CURRENT FILLNC DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 09/624,693
PRIOR FILING DATE: 2000-07-24
PRIOR APPLICATION NUMBER: PCT/US01/23270
                                                                                                                                                                                                                                          APPLICANT: Yoshida, Roberta
APPLICANT: Kootstra, Anna
TITLE OF INVENTION: Phenylalanine Ammonia Lyase Polypeptide and
TITLE OF INVENTION: Polynucleotide Sequences and Methods of obt
TITLE OF INVENTION: Using Same
FILE PEFEPENCE 29479/500NSCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FIRE MEFERENCE: 2024 (PARA-013PRV)
CURRENT APPLICATION NUMBER: US/09/770,149
CURRENT FILING DATE: 2001-01-26
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PRIOR FILING DATE: 2000-01-27
SOFTWARE: Patentin Ver.
                             PRIOR FILING DATE: 2001-07-24
NUMBER OF SEQ ID NOS: 30
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TYPE: DNA
OPGANISM: Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1952 CAAAAGATCGCTACCTTCGAAGAAGAAGTTGAAAGTCCTGTTACCGAAAGAAGTTGAAGGT 2011
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2072 TCGTACCCGFFGFAFAGGFFFGFAAGGGAGGAGCFCGGGCAGAGGGFFFFFFGACCGGAGAA 2131
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LOCATION: (1)..(2163)
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
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1380 AATTTTCTGAGCTGGTTAACGAITICTACAACAATGGATTACCATCGAATCTCTCCGGTG 1439
                                                    1271 CVAACACGATGGAGAAGACTCGCCTCGCVCTCGCCCTGATCGGCAAGCTCAACTTCACGC 1330
                                                                                                       1320 GAGTTTCCATGGACACACCCGTCTCGCCATTGCTGCAATCGGAAAACTCATGTTCGCTC 1379
                                                                                                                                                              1211 TCATCGACGTCGAGAACAAGAHGACCCACCACGGCGGCAACTTCCAGGCGDCCGCTGTCG 1270
                                                                                                                                                                                                                1260 TGATCGACGTTTCCAGAAACAAAGCTTTACACGGTGGTAACTTCCAAGGAACCCCAATCG 1319
                                                                                                                                                                                                                                                                     1151 ACATGATTCACGCCCACGCBGTCCTCCGCTCGAGGCCGAGTCGACGACCGACAACCCGC 1210
                                                                                                                                                                                                                                                                                                                                                                         1091 TCCGCCAGGACCGCTACCCGCTCCGCACGTCGCCTCAGTGGCTCGGCCCGCTCGTCAGCG 1150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        851 IGGGGACCCTCGCTCTGCACGACGCACACATGCTCTCGCTCCTCTCGCAGGGGTCACGG 910
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 20, Application US/09939408A Patent No. US20020102712A1
                                                                                                                                                                                                                                                                                                            Matches 645;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 29479/500NSCA
CURRENT APPLICATION NUMBER: US/09/939,408A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 09/624,693
PRIOR FILING DATE: 2000-07-24
PRIOR FILING DATE: 2001-07-24
PRIOR FILING DATE: 2001-07-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Phenylalanine Ammonia Lyase Polypeptide and TITLE OF INVENTION: Polynucleotide Sequences and Methods of Obtaining and TITLE OF INVENTION: Using Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 30 SOFTWARE: PatentIn Ver. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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OTHER INFORMATION: n = A or C or G or T; "n" indicates no consensus at that posit OTHER INFORMATION: Description of Artificial Sequence: Consensus

OTHER INFORMATION: Sequence of SEQ ID NOS: 12, 16, and 18
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                          669 ACATCACCCCTTGTTTACCCCCTCCGTGGAACCATCACCGCCTCCGGGTGACCTTGTCCCAT 728
                                                                                557 GCGGCCACTCGGCNGTCCGCCTCGTCGTCCTCGAGGCGCTCACCAACTTCCTCAACCACG 616
                                                                                                                                    609 AGGGTTACTCCGGCATCCGATTCGAGATCTTGGAAGCCATCACCAAGTTCCTTAACAACA 668
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                                                                       AAAAGGTCCTCACCATGGGCGTCAACGGCGAGCTCCACCGGTCGAGATTCTGCGAGAAAG 1796
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: APPLICANT: Yoshida, Roberta
: APPLICANT: Kootstra, Anna
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; Patent No. US20020102712A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Kootstra, Anna
TITLE OF INVENTION: Phenylalanine Ammonia Lyase Polypeptide and
TITLE OF INVENTION. Polynupleotide Sequences and Methods of Obtaining and
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LOCATION: (493)..(495)
OTHER INFORMATION: Other information:
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LOCATION: (37)..(2196)
NAME/KEY: modified_base
LOCATION: (494)
CTHEP INFORMATION: Other information: y = t or c
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                                                                                                                                                                          887 T3803ACCCCAGTCTGCACGACTCGCACAGTCGCACAGCTCTCGCACGCCTCTCGCAGGCCTTGACGG 946
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Local Similarity 52.2%;
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                            SOFTWARE: PatentIn Ver. SEQ ID NO 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 16, Application US/09939408A Patent No. US20020102712A1
                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/939,408A CURRENT FILING DATE: 2001-08-24 PRIOR APPLICATION NUMBER: US 09/624,693 PRIOR FILING DATE: 2000-07-24 PRIOR APPLICATION NUMBER: PCT/US01/23270
                                                                                                                                                                                                                                                                      APPLICANT: Yoshida, Roberta
APPLICANT: Kootstra, Anna
TITLE OF INVENTION: Phenylalanine Ammonia Lyase Polypeptide and
TITLE OF INVENTION: Polynucleotide Sequences and Methods of Obtaining
TITLE OF INVENTION: Using Same
FILE REFERENCE: 29479/500NSCA
                                                                                 PRIOR FILING DATE: 2001-07-24 NUMBER OF SEQ ID NOS: 30
     LENGTH:
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US-09-939-408A-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1143 AACAAGATCGTTATGCTCTCCGTACATCTCCCCAATGGCTCGGACC---TCAAATCGAAG 1199
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                                                                                                                                    AATTTTCTGAGCTGGTTAACGATTTCTACAACAATGGATTACCATCGAATCTCTCCCGGTG 1439
                                                                                                                                                                                                                                            GAGTTTCCATGGACAACACCCGTCTCGCCATTGCTGCAATCGGAAAACTCATGTTCGCTC 1379
                                                                                                                                                                                                                                                                                                     TGATCGACCTCGAGAACAAGATGACCCACCATGGCGGAGCCTTCATGGCGAGCAGCGTCG
                                                                                                                                                                                                                                                                                                                                                     TGATCGACGTTTCCAGAAACAAAGCTTTACACGGTGGTAACTTCCAAGGAACCCCAATCG 1319
                                                                                                                                                                                                                                                                                                                                                                                                          TGATTCACGCTCACGCTGTCCTCTCGCTCGAGGCTGGTCGAGTCGACCACCGACAACCCGC 1846
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TAATCCGATCATCAACCAAAATGATCGAGAGGGAAATCAATTCCGTCAACGACAACCCAT 1259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGCAGGACCGGTACCCGCTCCGCTGCTCGCCGCAGTGGCTCGGTCCCCTTGTCAGCGACA 1786
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTACTGTCGAGGCCATGGTCGGACACGCCGGCTCGTTCCACCCATTCCTCCACGACGTCA 1606
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Pred. No. 2e-45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 9.1%; Score 223.4; DB 10; Length 2061; Best Local Similarity 52.8%; Pred. No. Z Ze-44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/147,719 PRIOR FILING DATE: 1949-08-06
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846 TOGAGTTACAGCAGAAAAGAAAAAAAAATTAGCACTTGTTAACAGAAACGGCGCGCGAGGGCGGCGGGGGAAA 905
                                                                                                 623 AGGGCAAGGAGAAGATCCTGTACGCCCGAGGCGATGGCGCTCTTCTCAACCTCGAGCCCG 682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  503 GCATCACCCCCATCCTCCCCCTCCCCGGGGACCATCTCTGCGTCGGGGGGACCTGTCTCCTC 562
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                                                                                                                                                                                                                                                                                    TUTUUTAUATTIGUAGUGGA YATUAGUGGTUATUAGUGGAWAG YAAGGTGVAUGTUGTUUTAUG 622
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GENERAL INFORMATION:
APPLICANT: Tang, XIAO-Song
TITLE FE ENVENTION - BOPPODETION OF PAPA-HYDPOXYCINNAMIC ACID
FILE REFERENCE: BC1009 US CIP
CUPPENT APPLICATION NUMBER - US/09/765,873A
CURRENT FILING DATE: 2001-01-19

PRIOR APPLICATION NUMBER: US 09/627,216
PRIOR FILING DATE: 2000-07-27
PRIOR APPLICATION NUMBER: US 60/147,719

Sequence 7, Application US/09765873A Patent No. US20010053847A1

PRIOR FILING DATE: 1999-08-06 NUMBER OF SEQ ID NOS: 38

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; NAME/KEY: CDS
; LOCATION: (1)..(2151)
US-09-765-873A-7
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                                                                                                                                                                      CATTGATCGACGTTTCCAGAAACAAAGCTTTACACGGTGGTAACTTCCAAGGAACCCCAA 1316
                                               TGGCCAACACCATGGAGAAGACTCGCCTCGGGCTCGCCCAGATCGGCAAAGCTCAACTTCA 1312
                                                                                                                                                                                                                                                                                     AAGTAATCCGATCATCAACCAAAATGATCGAGAGGGAAATCAATTCCGTCAACGACAACC 1256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; NAME/KFY: CDS
; LOCATION: (1)..(2148)
US-09-939-408A-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 9.1%;
Best Local Similarity 52.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 18, Application US/09939408A Patent No. US20020102712A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 603;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Kootstra, Anna TITLE OF INVENTION: Phenylalanine Ammonia Lyase Polypeptide and TITLE OF INVENTION: Polynucleotide Sequences and Methods of Obtaining and TITLE OF INVENTION: Using Same FILE REFERENCE: 29479/500NSCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 09/624,693 PRIOR FILING DATE: 2000-07-24 PRIOR APPLICATION NUMBER: PCT/US01/23270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/939,408A CURRENT FILING DATE: 2001-08-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Yoshida, Roberta
APPLICANT: Kootstra, Anna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRIOR FILING DATE, 2001-07-24
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789 GAGAAGTCCTCAATGCCGAAAAGGCCTTCGCTGC---AGCCGGAGTTGAAGGTGGGTTCT 845
                                                    653 TCTCCTACATTGCAGCGGCCATCAGCGGTCACCCGGACAGCAAGGTGCAGGTCGTCCACG
                                                                                                      729 TATCATACATCGCCGGCCTCTTAACCGGCCGCCCAACTCCAAAGCCGTTGGCCCCACCG 788
                                                                                                                                                           593 GCATCACCCCCATCGTCCCCCTCCGCGGCACCATCTCTGCGTCGGGCGACCTCTCTCCTC
                                                                                                                                                                                                                                                                     533 GCGGCCACTCGGCTGTCCGCCTCGTCGTCGTCGAGGCGCTCACCAACTTCCTCAACCACC 592
                                                                                                                                                                                                                                                                                                                          609 AGGGTTACTCCGGCATCCGATTCGAGATCTTGGAAGCCATCACCAAGTTCCTTAACAACA 668
                                                                                                                                                                                                                                                                                                                                                                            473 ACTCGCTTCCCCTCGAGGTTGTTCGCGGCGCCATGACAATCCGCGTCAACAGCTTGACCC 532
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GENERAL INFORMATION:
APPLICANT: Tang, Xia
ITITLE OF INVENTION:
FILE REFERENCE: BCIO
CURRENT APPLICATION
                                                                                                                                                          RESULT 14
US-09-765-873A-9
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                                                                                                              ; Sequence 9, Application US/09765873A
; Patent No. US20010053847A1
                     TITLE OF INVENTION GLOPPOPHOTION OF FARA HYDROXYCINNAMIC FILE REFERENCE: BC1009 US CIP
  CURRENT APPLICATION NUMBER: US/09/765,873A
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                                                                 Xiao-Song
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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PRIOR APPLICATION NUMBER: US 09/627,216
PRIOR FILING DATE: 2000-07-27
FPIOR APPLICATION NUMBER: US 60/147,719
PRIOR FILING DATE: 1999-08-06
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NAME/KEY: CDS
LOCATION: (1)..(2151)
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TYPE: DNA
                                                    1193 CTCTCATOSACHTOGAGAAVAAVACITOGAGACACGOGGGAATTTCCAGGTGCGCTG 1252
                                                                                                                                                                                                                                                              1317 TCGGAGTTTCCATGGACAACACCCCTCTCGCCATTGCTGCAATCGGAAAACTCATGTTCG 1376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                549 ACACACTTCCACATTCAGCCACTAGAGGGGGGGGGGGATGATGATGAGAATGAAGAGGCTGCTGC 608
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                                                                                                         CATTGATCGACGTTTCCAGAAACAAAGCTTTACACGGTGGTAACTTCCAAGGAACCCCAA 1316
                                                                                                                                                          AAGTAATCUGATCAACCAAAATGATCGAGAGGGAAATCAATTCCGTCAACGACAACC 1256
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; Patent No. US20020110548A1
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LENGTH: 363
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FILE REFERENCE: 38-21(15401)B
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Byrum, Joseph R. APPLICANT: La Rosa, Thomas J. APPLICANT: Thompson, Michael D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Glycine max OTHER INFORMATION: Clone ID: LIB3028-013-Q1-B1-G3
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                         1658 CTATGCCAATCCATCGATTTACGCCATTTGGAAGAGAACATGAAATCGACAGTGAAGAAC 1717
                                                                                                                         1598 AGGAAAACCGCAGAAGCAGTCGACATCTTAAAACTCATGTCGTCGACATACTTAGTCGCT 1657
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                                                                                                                                                                                                                                                                           62 GAAATTGCCATGGCATCTTATTGTTCTGAACTTCAATATTTGGCGGAATCCGGTGACAAGC 121
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  0; Mismatches 102; Indels
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Search completed: March 29, 2003, 02:08.56 Job time : 213 secs

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Result
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     IIS-09-615-192A-245
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Sequence 14, Appl
Sequence 26, Appl
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Sequence 12, Appl
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                                                                         GENERAL INFORMATION:
APPLICANT: Bloksberg, Leonard N. APPLICANT: Havukkala, Ilkka TITLE OF INVENTION: Materials and
                                                                                                                                                                                                                                                                                                                                                                                                             1310 ACCCCAATCGGAGTITCCATGGACAACACCCGTCTCGCCATTGCTGCAATCGGAAAAACTC 1369
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PRIOR FILING DATE: 1997-11-21
PRIOR FILING DATE: 1996-09-11
PRIOR FILING DATE: 1996-09-11
PPTOP APPLICATION NUMBER US 09.
PRIOR FILING DATE: 1998-10-09
PRIOR FILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 405
SOFTWARE: FastSEQ for Windows V.
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LENGTH: 1520
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ORGANISM: Pinus radiata
                                                       1434 CCGGTGGACGTAACCCTAGTTTGGACTACGGGTTCAAAGGTGGAGAAATCGCCATGGCTT 1493
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Local Similarity 67.2%;
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GTGGTGGGCCTAATCCCAGCCTGGATTATCGACTGAAAGGGGCCCGAGATCGCTATGGCTT 776
                                                                                                                                               TCGCTCAATTTTCTGAGCTGGTTAACGATTTCTACAACAATGGATTACCATCGAATCTCT 1433
                                                                                                                                                                                                                        CTATTGGTGTTTCCATGGATAATCTTCGTCTGTCAATTTCAGCAATTGGGAAATTGATGT 656
                                                                                                                                                                                                                                                                             CAATCGGAGTTTCCATGGACACACCCGTCTCGCCATTGCTGCAATCGGAAAACTCATGT
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                                                                                                               TCGCTCAATTCTCAGAGCTTGTGAATGATTACTACAATGGAGGCTTGCCTTCGAATCTGA 716
                                                                                                                                                                                                                                                                                                                                        ATCCAGTAATTGATGTTGCCAGAGACAAAGCTCTACATGGAGGGAATTTCCAGGGCACAC 596
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                                            ; TYPE: DNA; ORGANISM: Eucalyptus grandis US-09-615-192A:244
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  Query Match
                                                                                                                                   SOFTWARE. F
SEQ ID NO 244
                                                                                                                                                                                                                                             PRIOR FILING DATE: 1997 11 21 PRIOR APPLICATION NUMBER: US (PRIOR FILING DATE: 1996-09-11
                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/615,192A CURRENT FILING DATE: 2000-07-12
                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Materials and methods for the TITLE OF INVENTION: Modification of Plant Lignin Content
                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Bloksberg, Leonard N. APPLICANT: Havukkala, Ilkka
                                                                                                                                                                                                PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1998-1
                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 08/975,316
                                                                                                                                                                              NUMBER OF SEQ ID NOS:
                                                                                                              LENGTH: 681
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Score 362.6;
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                                                                                                                   SOFTWARE: |
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                                                                                                                                                                                        PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 2000-
                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/545,686 CURRENT FILING DATE: 2000-04-07
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                                                                                                                                                              NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                            FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                APPLICANT: Gaitan, Alvaro L.
TITLE OF INVENTION: CONSTITUTIVE AND INDUCIBLE PROMOTERS FROM COFFEE PLANTS
                                           ORGANISM. Phenylalanine Ammonia Lyase Consensus Sequence
                                                                  LENGTH: 500
TYPE: DNA
NAME/KEY, unsure
                         FEATURE:
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Best Local Similarity 70.7%; Pred. No. 4.3e-60;

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: OTHER INFORMATION: N at any position in this sequence is either A, C, ; OTHER INFORMATION: G, or T. US-09-545-686-12
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                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 08/975,316
PRIOR APPLICATION NUMBER: US 08/975,316
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: US 08/713,000
PRIOR FILING DATE: 1996-09-11
PRIOR APPLICATION NUMBER: US 08/713,000
  Query Match
                                                                                                                                                    SEQ ID NO 97
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                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US (PRIOR FILING DATE: 1998-10-09 NUMBER OF SEQ ID NOS: 405
                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Materials and Methods for the TITLE OF INVENTION: Modification of Plant Lignin Content
                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/615,192A CURRENT FILING DATE: 2000-07-12
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APPLICANT:
                                                                                                                                                                               SOFTWARE:
                                                                           TYPE: DNA ORGANISM: Pinus radiata
                                                                                                                          LENGTH: 577
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                                                                                                                                                                               FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Havukkala, Ilkka
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  Score 274.4;
  DB 4;
Length 577;
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                 FILING DATE: September 11, 1996
ATTORNEY/AGENT INFORMATION:
NAME: SLEATH, Janet
REGISTRATION NUMBER: 37,007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: BLOKSBERG, Leonard N., HAVUKRALA, Iİkka APPLICANT: and GRIERSON, Alastair W.
TITLE OF INVENTION: MATERIALS AND METHODS FOR TITLE OF INVENTION: THE MODIFICATION OF PLANT LIGNIN CONTENT NUMBER OF SEQUENCES: 88
                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                     AFPLICATION NUMBER:
                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                      COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Law Offices of Ann W. Speckman STREET: 2601 Elliott Avenue, Suite 4185
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REFERENCE/DOCKET NUMBER:
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11000/1003C1
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                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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                                                                                                                      CURRENT APPLICATION NUMBER: US/09/615,192A
CURRENT FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 08/975,316
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: US 08/713,000
                                                                                                                                                                                                                                                                                                                                 APPLICANT: Bloksberg, Leonard N. APPLICANT: Havukkala, Ilkka
                                                                                                      PRIOR APPLICATION NUMBER - PRIOR FILING DATE: 1996-0
                                                                                                                                                                                                                                                             FILE REFERENCE:
                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Materials and Methods for the TITLE OF INVENTION: Modification of Plant Lignin Content
                                                   PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1998-
                          NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO.
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LENGTH: 684 base pairs
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TELEPHONE: 206-269-0565
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FastSEQ for Windows Version 3.0
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APPLICANT: YOShida, Roberta
APPLICANT: YOShida, Roberta
APPLICANT: KOLStra, Anna
TITLE OF INVENTION: Phenylalanine Ammonia Lyase Polypeptide and
TITLE OF INVENTION: Polynacleotide Sequences and Methods of obtaining and
TITLE OF INVENTION: Using Same
FILE REFERENCE: 29479/500NSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-624-693A-20
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                                                                                                                                                                                                                                                                            ; SEQ 110 NO 20
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Patent No. 6355468
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                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/624,693A CURPENT FILING DATE: 2000-07-24 NUMBER OF SEQ ID NOS: 25
                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Ver. 2.0
FEATURE: misc_difference NAME/KEY: misc_difference LOCATION: (13, 34, 46, 49, 51, 57, 59, 68, 69, 73, 75 - 77, 79, 82, 84, LOCATION: n = A or C or G or T; "n" indicates no consensus at that posit OTHER INFORMATION: Description of Artificial Sequence: Consensus OTHER INFORMATION: Sequence of SEQ ID NOs: 12, 16, and 18
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TYPE: DNA
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1317 TCGGAGTFTCCATGGACAACACCCGTCTCGCCATTGCTGCAATCGGAAAACTCATGTTCG 1376
                                                                                                   1394 CTGCCGAGGACCCNTCGCTCTCCTATCACTGCAAGGGCCTCGACATTGCCGCNGCNGCNT 1453
                                                                                                                                                    1437 GTGGACGTAACCCTAGTTTGGACTACGGGTTCAAAGGTGGAGAAATCGCCATGGCTTCTT 1496
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PRIOR FILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 405
SOFTWARE: FASLSEQ for Windows
SEQ ID NO 242
SEQ ID NO 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/615,192A CURRENT FILING DATE: 2000-07-12 PRIOR APPLICATION NUMBER: US 08/975,316 PRIOR PILING DATE: 1997-11-21 PRIOR APPLICATION NUMBER: US 08/713,000 PRIOR FILING DATE: 1996-09-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Bloksberg, Leonard N.
APPLICANT: Havukkala, 11ka
TITLE OF INVENTION: Materials and Methods for the
TITLE OF INVENTION: Modification of Plant Lignin Content
FILE REFERENCE: 11000.1003cdU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
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2120 TIGACCGGAGAAAAGGIGACGICGCCGGGAGAGGAGIITUGACAGGGIGITUACGGCGAIG 2179
                                                                                                                                                                                                                                                                                                                          1940 ACCTCCATCTTCCAAAAGATCGCTACCTTCGAAGAAGAATTGAAAGTCCTGTTACCGAAA 1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1760 AACGGCGAGCTCCACCGGTCGAGATTCTGCGAGAAAAATCTCCTCCGTGTTGTTGATCGT 1819
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                                                                                                              2060 AAAGCTTGCAGATCGTACCCGTTGTATAGGTTTGTAAGGGAGGAGCTCGGCAGAGGGTTT 2119
                                                                                                                                                                                                                                2000 GAAGTTGAACGTGTTAGAATCGCTTATGAGAATGATACATTGTCGATTCCAAACAGGATT 2059
                                                                                                                                                                                                                                                                                                                                                                                                                                                              1880 CTCCGACAGGTTCTGGTCGACCACGCTCTAAACAACGGCGAAACGGAGAAGAACACTAAC 1939
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                                                        242 GACGTCGAGGGCGTTCGAGTCCAGTACGAGACAGGCAACCTCGCCATCCCCAACCAGATC 301
                                                                                                                                                                                                                                                                                         182 ACTTCGATCTTCCAAAAGATCGTGGCCTTCGAGGAGGAGCTCAAGGCCCAGTTGCCGAAG 241
                                                                                                                                                                                                                                                                                                                                                                                                        122 CTGAGGCAAGTCCTGGTCGACCAGGCACTGGTGAATGGCGAGGGGAGCTGAACCCGAGC 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Watch 10.2%; Score 250; DB 4 Local Similarity 68.9%; Pred. No. 7e-54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 GAGCATGTGTTTACCTACGCTGATGACGCCTGCAGCGCCACCTACCCGCTGATGCAGAAG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 AATGGCGAGCTCCACCGTCTCACTACTGTGAGAGGGACCTGCTCAAAGTGGTCGACCGC 61
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US-09-624-693A-12
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APPLICANT: Yoshida. Roberta
APPLICANT: Yoshida. Roberta
APPLICANT: State Anna
TITLE OF INVENTION. Phenylalanine Ammonia Lyase Polypeptide and
TITLE OF INVENTION. Polynucleotide Sequences and Methods of Obtaining and
TITLE OF INVENTION: Using Same
FILE REFERENCE: 29479/500NSC
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CUPRENT FILING DATE: 2000-07-24
NUMBER OF SEQ ID NOS. 25
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    1026 TGAAGCAT -- - CACCCTGGTCAAATCGAGGGGGGGGGGGATCATGGA - - GTATATTTTGG 1079
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    482 CTTCCCATCTCTTAGGAA 499
                                                                                                   947 CTCTCACGGTGGAGGCCATGGTCGGCCAGCAGCAGGCTCGTTCGCCCCGTTCATCCACGACG 1006
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             549 ACACACTTCCACATTCAGCCACCAGAGCCGCCATGATCGTCAGAATCAACACCCTCCTCC 608
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                                                                                                                                                                                            CGATCTTCGCTGAGGTTATGCAAGGGAAGCCGGAGTTTACCGATCACTTGACACACAAAT 1025
                                                                                                                                                                                                                                                                                                                                                                               TGGCTTCCATGGTTCTATTTGATGCTAATGTACTTGCGTTGTTGTTCGGAAGTGTTATCGG 965
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACACGCTTCCGCTCGAGGTCGTCCGCGGCGCCATGGTCATCCGCGTCAACTCGCTCACGC 586
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Fred. No. 4.3e·52;
0; Mismatches 575; Indels 12; Gaps
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: HAVUKKAIA, IIKKA
APPLICANT: GELECSON, ADASLAIR
TITLE OF INVENTION: MATERIALS AND METHODS FOR THE
TITLE OF INVENTION: MODIFICATION OF PLANT LIGNIN CONTENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1740 AGGTOCTCACCATGGGGGTCAACGGCGA 1767
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                                                                                                                                                                                                                                                         Sequence 9, Application US/08975316 Patent No. 5952486
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                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 206-269-0563 INFORMATION FOR SEQ ID NO: 9:
                                                                                 APPLICANT: BLOKSBERG, Leonard N., HAVUKKALA, IIkka APPLICANT: and GRIERSON, Alastair W. TITLE OF INVENTION: MATERIALS AND METHODS FOR TITLE OF INVENTION: THE MODIFICATION OF PLANT LIGNIN CONTENT NUMBER OF SEQUENCES: 88

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1205 CGATCATCAACCAAAATGATCGAGAGGGAAATCAATTCCGTCAACGACAACCCATTGATC 1264
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TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                 589 GATGTCTCCAGGGACATGGCTGTCCACGGCGGCAAC 624
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                      STREET:
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                                                                  ADDRESSEE:
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                                                                Law Offices of Ann W. Speckman
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Sequence 9, Application US/09211710A; Patent No. 6204434; GENERAL INFORMATION; APPLICANT
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM:
SUFTWARE: FastSE
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Local Similarity 69.7%;
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                                                                                                                                                                                                                                                                                   CGATCATCAACCAAAATGATCGAGAGGGAAATCAATTCCGTCAACGACAACCCATTGATC 1264
                                                                                                                                                                                                                                                                                                                            CAAGACCGCTACGCTCTGCGAACATCGCCACAGTGGTTGGGGGCCTCCGATCGAAGTCATC 528
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CURRENT APPLICATION NUMBER: US/09/615,192A
CURRENT FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 08/975,316
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: US 08/713,000
PPIOR FILING DATE: 1996-09-11
PRIOR APPLICATION NUMBER: US 09/169,789
PRIOR FILING DATE: 1998-10-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 9, Application HS/09615192A Patent No. 6410718
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COPPENT FILING DATE: 1998-12-14
NUMBER OF SEQ ID NOS: 15
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APPLICANT: Grierson, Alastair
TITLE OF INVENTION: Materials and Methods for the
TITLE OF INVENTION: Modification of Plant Lignin Content
FILE REFERENCE: 11000.1003c3
                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Materials and Methods for the TITLE OF INVENTION. Modification of Plant Liquin
SOFTWARE:
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                                             NUMBER OF SEQ ID NOS.
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ORGANISM: Pinus radiata
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                      FastSEQ for Windows Version 3.0
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Havukkala, ilkka
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                                                                                                                                              ; NAME/KEY: CDS
; LOCATION: (646)..(2784)
US-U9-524-593A-16
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APPLICANT: Yoshida, Roberta
APPLICANT: Yoshida, Roberta
APPLICANT: KOUStra, Anna
TITLE OF INVENTION: Phenylalanine Ammonia Lyuse Polypeptide and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 16, Application US/09624693A
; Patent No. 6355468
                                                                                                                                                                                                                                                                         SEQ ID NO 16
LENGTH: 2787
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                                                                 Matches
                                                                                 Query Match 9.3%;
Best Local Similarity 52.5%;
                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Polynucleotide Sequences and Methods of Obtaining and TITLE OF INVENTION: Using Same FILE REFERENCE: 29479/500NSC
                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/624,693A CUPPENT FILING DATE: 2000-07-24
                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 25
                                                                                                                                                                                                                       TYPE: DNA
OFGANISM: Fhodotorula mucilaginosa
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549 ACACACTTCCACATTCAGCCACCACCAGCAGCCCCCATCATCGTCAGAATCAACACCCCTCCTCC 608
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                                                                 648;
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                                                             0; Mismatches 565;
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                                                                                 Score 228; DB 4; Length 2787; Fred. No. 5.1e-48;
                                                             Indels
                                                             21;
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1136 ACTOGCTTCCGCTCGAAGTCGTCCGAGGCGATGACCATCCGTGTCAACTCGCTCACTC 1195

Qy Qy Db

Qγ

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2204 ACGITCICICCICCICCICGCCACCIACCIITACIGCGCCICCAGGCCGICGACCICC 1263
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                                                                                                                                                                                             1560 ACAATCAAGACGTTAATTCTCTCGGATTAATTTCAGCGAGGAAAACCGCAGAAGCAGTCG 1619
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Βb

В 200 Вb Qγ Ър Qy Ъ QY D) 9 DЬ Qy Дb QΥ В 2 DЪ Qy Ъ Qy

Qy 1740 AGTCCTRCACCATGGGCGTCAACGGCGCTCA 1773
Db 2324 AGCACTTTGGCGGCGTCGACGGCGAAGTCGA 2357

Search completed: March 28, 2003, 23:41:49 Job time : 119 secs

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Database
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Perfect score:
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10804.283 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		Ouerv				
N ○.	Score	Match	Match Length DB		19	Description
_	2442	100.0	12442	ا د	ABK 50679	cDNA encoding lett
N	1603.8	65.7	2380	24	ARKSOKRO	CDNA encoding lett
w	1215.8	49.8	2400	21	WC 21 cce	Arabidopsis thalia
4	1204.6	49.3	2370	21	AAC45027	Arabidopsis thalia
Ţ	1200.6	49.2	2012	<u>.</u>	AAC39455	Arabidopsis thalia
	1159	47.5	2607	14	AAQ31985	Pisium sativum L P
7	1095	44.8	2211	1.3	AAC51293	Arabidopsis thalia
	1005.2	41 2	5291	11	AAQ05768	GPAL2 promoter.
/	972.4	39.8	4415	21	AAC61194	Pea PSPAL1 DNA seq

Saltveit M,

Campos P, Nonogaki II,

Suslow

(REGC) UNIV CALIFORNIA. 26-SEP-2000; 2000US-235956P 26-SEP-2601; 2001W0-HS30192

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2787 2787 2061 2151 2151 2151 2151 2328	2419 6244	684 688 688 688 688 688 688 688 688 688	791 753 748 759 759 696	4415 3438 1707 1455 1503 1520 1475
44444 94444	144140	19 21 24	3 4 4 4 4 C C	114 124 124 124
AAA67916 ABA65242 ABA95242 AAB33095 AAB33097 AAB33097 AAB33097 AAB33097	AACQ35213 ABAQ55244 ABAQ5528 AAAA68149 ABAQ5240 AAAACA3916	AAV23865 AAX206898 AAA6586 AAA67952 ABN87233 ABN87233	ARM87224 ARM87225 AHM87225 ADAGA151 ADAG8232 ADB097227 ABC87227 ABC87227	AAQ46293 AAQ05764 AAQ33019 AAA68152 AAH87223 AAAF8154 AAAF8154 AAAF87231
Fine phenylaranine Finus radiata PAL Finus radiata PAL R. rubra/mucilagin Rhodotorula glutin Rhodotorula glutin R. glutinis phenyl Rhodotorula glutin Sequence of Rhodos	Zoa mays DNA fragm Rhodotorula PAL co Lolium perenne LpP Facelyptus grandis R. graminis PAL po Plant PAL cnzyme D	Plant PAL chzyme D Pine phenylalanine Pinus radiata phen Pinus radiata ph. Lolium perenne Lpe Arabidopsis thalia	Lolium perenne Lpp Lolium perenne Lpp Lolium perenne Lpp Eucalyptus grandis Lolium perenne Lpp Lolium perenne Lpp Atabidopsis thalia Pinus radiata PAL	עס ס ד

ALIGNMENTS

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RESULT 1
ABK50679
CDS
                                         04-APR-2002.
                                                                                                                                        Lettuce; phenylalanine ammonia·lyase; plant wounding; plant damage; plant disease; plant browning, vegetable crop; plant; LsPAL1;
                                                                                                                                                                                                                     ABK50679 standard; cDNA; 2442 BP
                                                         W0200226028-A2
                                                                                                                  Lactuca sativa
                                                                                                                                                                   cDNA encoding lettuce LsPAL1 enzyme
                                                                                                                                                                                  13-AUG-2002 (first entry)
                                                                                        Location/Qualifiers
                                                                        /*tag- a
/product= "LsPAL1"
                                                                                  /*tag-
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QY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the preparation of plant expression constructs for modifying features of the response of a plant cell to wounding, damage or other injury from disease. Disruption or down-regulation of PAL activity can be used to reduce the browning response to wounding in vegetable crops. The present sequence encodes lettuce LSPAL1 enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Lactuca sativa) phenylalanine ammonia-lyase (LsPAL) enzymes, and the polynuclectide sequences encoding them. An antibody that binds to a PAL enzyme is useful for measuring the relative amount of PAL levels in a tissue. The polynucleotide sequences encoding PAL are useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Fig 5; 46pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel polynucleotide useful in preparing plant expression constructs to modify the response of a plant cell to wounding damage or other injury from disease causing organisms or from plant posts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WFI; 2002-435152/46.
P-PSDB; AAU97130.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2442 BP; 693 A; 553 C; 592 G; 604 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to the isolation of movel lettuce
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 100.0%; Score 2442;
Local Similarity 100.0%; Pred. No. 0
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                                                                                                                                                                                  AACAAGCCACACACTTCCACATTCAGCCAGCAGAGCCGCCATGATCGTCAGAATCAACAC 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAUGGCTGGAGTTAAGGCGAGTAGTGATTGGGTTATGGAGAGCATGAATAAAGGAACTGA 420
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                                                                  CCTCCTCCAGGGTTACTCCGGCATCCGATTCGAGATCTTGGAAGCCATCACCAAGTTCCT
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plant disease, plant browning, vegetable crop, plant; LsPAL2;
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/product- "LsPAL2"
/transl_except~ (pos:135..145, aa:Val-Gly)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel polynucleotide useful in preparing plant expression constructs to modify the response of a plant cell to wounding, damage or other injury from disease causing organisms or from plant pests
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     can be used to reduce the browning response to wounding in vegetable crops. The present sequence encodes lettuce LsPAL2 enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2380 BF; 663 A, 548 C, 603 G; 566 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 2; Fig 7; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to the isolation of novel lettuce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; AAU97131.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                169 GGATOTATTGAACTGGGGGAGTTGCAGCGGAGGGGGTGACCGGGAAGTCACCTTGATGAGGT
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TTGCAGCGCACATACCCATTAATGCAGAAGCTCCGACAGGTTCTGGTGGACCACGCTCT
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                                                                                                                                 CGAGAAAGATCTCCTCCGTGTTGTTGATCGTGAATACGTCTTCGCTTACATCGACGACGT 1848
                                                                                                                                                                                                          CGTCGCGAAGAAGATCCTAACCACCGGCGTCAATGGCGAGCTCCACCCTTCTCGCTTCTG
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                                                                               860 AAAGAAGGGCTAGCACTTGTTAACGGCACCGCGTGGGGTCCGGGATGGCTTCCATGGTT 919
                                                                                                                       802 ACCGCGAAAGAAGCTTTTGAGAAAGCCGGAATCAGTACTGGATTCTTCGATTTACAACCT 861
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                 1068 AGTATATTTTGGACGGAAGCGATTACGTCAAGGCGGCGCAAAAGGTCCACGAAAATGGACC
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                                                  ATCATCTCACTCACAGACTTAAACATCATCCCGGTCAAATCGAAGCGGCGGCGATAATGG
                                                                                  ATCACTTGA/ ACA/ AAATTGAA//CATCA/CC/TG/JTCAAATC/AA/GC/A/GC/GA/CATCAT/G
                                                                                                                                                                                      CGGCGGTTGGATCTGGAATGGCGTCAATGGTGTTATTCGAAACGAATGTTCTCTCTGTTT
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s-0159330. s-0159331. s-0159637.

S-0158369. S-0159293. S-0159294. S-0159295. S-0159329.

S-0158029. S-0158232.

S-0159638. S-0159584. S-0160741. S-0160767.

3-0160768. 3-0160770.

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GAGAGGAGTTCGACAGGGTGTTCACGGCGATGTGCAAAAGGTCAAATTATTGATCCGTTGT 2207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCGAGAAAGATCTCCTCCGTGTTGTTGATCGTGAATACGTCTTCGCTTTACATCGACGACG
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200 GCGTTGACCGGAAGTCACCTTGATGAGGTGAAGAAGATGGTTGCGGAGTTCAGAAAGCCG
                        150 AAAGTGGCGGTTACTACGAAGACTTTGGCAGATCCATTGAATTGGGGTTTAGCAGCGGAT 209
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	ATCGAC HILLI ATCGAT	
	CGTACATCTCCCCAATGGCTCGGACCTCAAATGGAAGTAATCCGATCATCAACCA 	1160 1163
1159 1162	AGAAACCAA            AGAAACCAA	
1099 1102	NATYATESHASTATATTTTGSACGGAAGGGATTACGTCAA 	1040
1039 1042	CCGGAGTFTACCGATCACTTGACACACAATTGAAG 	980 983
979 982	ACTTOCOTTOTTOTCOGAAGTOTTATCGCO 	920 924
919 923	IGTTAACGG ACCGCCGTTGGGTCCGG 	860 864
859 863	AGGCCTTCGCTGCAGCCGGAGTTGAAGGTGGGTTCTTCGAGTTACAGC 	800
799 803	300G0000AACTOCAAAG00GfTGG000CACGGGAGAAGT0CT 	740 744
739 743	ATCACOSCITOSARGACETTGTCCCATTATCATACA 	680 684
679 683	CATICCGATTICGAGATCTTIGGAAGCCATCACCAAGTTICCTTAACAACACAAC	620 624
619 523	COTCAGAATCAACACCCTCCTCC 	560 564
559 563	TTAGATTTTFGAACGCGGGAATATTCGGCAATGG 	50n 504
499 503	AACTAAGGAAGGGGGGGGTTTAGAGAAGGAGG 	440
439 443	GAATAAAGGAAC }              GAACAAAGGTAC	380 384
379 383	STGACACCCTBANGERGANCETTAAG 	320 324
319 323	STAGTAGAGAGATGC HAPAGHTHOTYAJGTIGOTGGGGATATOT 	260 270
697	GAAGTCATTTAGATGAA	210

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1403 GATTTOTACAACAATGGACTTOTTTCGAATCTAACTGCTTTCGAGTAATCCAAGTTTGGAT 1462
2303 AATTITAATTITGCTGT 2319
                                                                                                                                                                                                                                                        2240 CTTCCAATATGITAGGAAAGTGAGTGAAACGGTTTGAATTGIAITGTAATATTCTGI 2299
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                                                                                                                                                                TGTGAAGGTAAACTTATTGATCGTTGATGGATTGTCTCAAGGAATGGAACGCAGCTCCC 2242
                                                                                                                                                                                                                                                                                                                                                                                             TGCAAACGTCAAATTATTCATCCGTTGTTTGGAGGGTGGAGGGTGGAATGGGGAACCT 2239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAGGAATGTAGGTGGTATCCGTTGTATAGGTTTGTGAGGGAAGAGCTTGGAACGAAGTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAAGTTGAAGCGGCTAGAGCAAGCTTATGGGAACTGGAACTGCGATTCCTAACCGGATT
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Matches 1587; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence is that of the phenylalanine ammonia lyase (PAL) gene from Pisum sativum L. The gene may be used to produce PAL recombinantly. Plants contg. the PAL gene can contain a large amt. of phenyl propanoid isoflavonoid.

See also AAQ33019.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2607 BP; 795 A; 485 C, 577 G, 750 T; 0 other;
                          530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New phenylalanine ammonia lyase gene from Pisum sativum L -plasmid contg. gene, and E.\ coli\ transformed\ with plasmid, for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    prepn. of lyase.
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                                                                                                                                                                                                                                                                     441 AAGCGTATGGTGGAGGAGTACAGGAAGCCGGTGGTCCGCCTTGGTGGCGAGACACTGACG 500
                                                                                                                                                                                                                                                                                                                                                    170 GATCCATTGAACTGGGGAGTTGCAGCGGAGGCGTTGACCGGAAGTCACCTTGATGAGGTG 229
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                                                                                                                                                                       350 TCGGAAGCCGCGAGGGCTGGAGTTAAGGCGAGTAGTGATTGGGTTATGGAGAGCATGAAT 409
                                                                                                                                                                                                                                         290 GTTTCTCAGGTGGGGGGATCGCAGCTGCTAATGACAGTGACAGCGTGAAAGGTGGAGCTG 349
                                                                                                                                                                                                                                                                                       381 GATCCTTTGAATTGGGGTGTTGCCGCCGAGGCAATGAAAGGGAAGTCACTTGGATGAGGTG 440
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              AATGGAACGGAAACAAGCCACACACTTCCACATTCAGCCACCAGAGCCGCCATGATCGTC 589
                                            AAACAAGGTGGTGCTTTGCAGAAAGAACTCATCAGGTTTTTGAATGCTGGAATATTTGGA 734
                                                                                                                                                        TCAGAATCTGCTAGGGCTGGCGTTAAGGCGAGCAGTGACTGGGTGATGGAGAGTATGAAC
                                                                                                                                                                                                                ATTTCTCAGGTGGCTGCCATTGCCGCACATGATCATGGT-----GTTAAGGTGGAGTTG
                                                                AAGCAAGGCGGTGCTTTACAGAAGGAGCTCATTAGATTTTTGAACGCCGGAATATTCGGC
                                                                                                  AAAGGCACAGACAGTTACGGTGTTACTACCGGTTTCGGCGCGCCACCTCTCACCGGAGAACC
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           sativum
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Location/Qualifiers 126..2456
                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches 625;
                                                                                                                                                                                                                                                                                                                                                                                                  Score 1159; DB 14; Pred. No. 1.8e-198;
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                       1607 GCAGAAGCAGTCGACATCTTAAAACTCATGTCGTCGACATACTTAGTCGCTGTATGCCAA 1666
                                                                                                                                                                 1692 GCTTCTTATTGTTCTGAGTTACAATATCTTGCAAACCCAGTTACAACTCATGTTCAAAGT 1751
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                                                                                                                          GCCG---AACAACACAATCAAGACGTTAATTCTCTCGGATTAATTTCAGCGAGGAAAACC
                                                                                  GCTGAGCAACACAACCAAGATGTGAACTCTTTGGGTTTGATATCTTCTAGGAAAACA
                                                                                                                                                                                                          CTCTCCGGTGGACGTAACCCTAGTTTGGACTACGGGTTGAAAGGTGGAGAAATCGCCATG
                                                                                                                                                                                                                                                                                                                                    TICTTTGCTCAATTCTCTGAACTCGTCAATGATTTTTACAACAACGGGTTGCCTTCGAAT 1631
                                                                                                                                                                                                                                                                                                                                                                                                                     ACACCTATTGGTGTATCCATGGATAATACACGTTTGGCTCTTGCGTCAATTGGTAAACTC
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     06-SEP-2000
                                                                                                                Hybridisation assay: genetic mapping; gene expression control; protein identification; signal transduction pathway;
                                                                                                                                                                  Arabidopsis thaliana DNA fragment SEQ ID NO: 67981
                                                                                                                                                                                                                                                                 AAC51293 standard, DNA, 2211 BP
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                                      EP1033405-A2
                                                                   Arabidopsis thaliana.
                                                                                                  metabolic pathway, promoter, termination sequence; ss
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control of a promoter, using Agrobacter tumefacters (pref. LH4404) as a vector. Sequence inhibits lighin biosynthesis in the plant improving digestibility of animal foder, and useful in production of paper pulp etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antisense CAD gene tragment is inserted into the plant under the
                                                                                           Disclosure; Fig 6; 42pp; English
                                                                                                                       Recombinant DNA, for plants with reduced lignin content - improved animal fodder and paper pulp prodn.
                                                                                                                                                                        WP1: 1990-261294/35
                                                                                                                                                                                                                                                                                               14-DEC-1989;
                                                                                                                                                                                                                                                                                                                              15-JUN-1990.
                                                                                                                                                                                                                                                                                                                                                           CA2005597-A
                                                                                                                                                                                                                                                                                                                                                                                         SR1; Agrobacterium tumefaciens; lignin; ds;
                                                                                                                                                                                                                                                                                                                                                                                                                      GPAL2 promoter
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                                                                                                                                                                                                    Schuch WW, Knight ME,
                                                                                                                                                                                                                                   (SCHU/) SCHUCH W W.
                                                                                                                                                                                                                                                                  15-DEC-1988;
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                                                                                                                                                                                                                                                                  88GB-0029298
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                                                                                                                                                                                                     Edwards KJ,
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                    1461 ACGGGTTCAAAGGTGGAGAAATCGCCATGGCTTCTTACTGTTCTGAGGTTCAGTTTCTGG 1520
                                                                                                                                                                                                        4156 AGGCCTTGCATGCTGGTAACTTCCAAGGAACTCCAATTGGAGTCTCCATGGATAACACCC
                                                                                                                                                                                                                             4096 CAATTGAGAGGGAGATCAACTCAGTCAATGACAACCCTTTGATTAGTGTGTCTAGGAACA 4155
                                                                                                                                                                                                                                                                                                               1221 TGATCGAGAGGGAAATCAATTCCGTCAACGACAACCCATTGATCGACGTTTCCAGAAACA 1280
                                                                                                                                                                                                                                                                                                                                                                        1161 TCGGTACATCTCCCCAATGGCTCGGACCTCAAATGGAAGTAATCCGATCATCAACCAAAA 1220
                                                                                                                                                                                                                                                                                                                                                                                                                            3976 CTGCTAAGAAGTTGCATGAGATAGATCCTTTGCAGAAACCCAAACAAGATCGCTATGCCC 4035
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1101 CGGCGCAAAAGGTCCACGAAATGGACCCGTTACAGAAACCAAAACAAGATCGTTATGCTC 1160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1041 GTCAAATCGAGGCGGCGATCATGGAGTATATTTTGGACGGAAGCGATTACGTCAAGG 1100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             / Match 41.2%; Score 1005.2; DB 11; Length 5291; Local Similarity 73.3%; Pred. No. 6.6e-171;
                                                         ACTATTACAATAATGGGTTGCCTTCTAATCTCACTGCCAGCAGAAACCCCCAGCTTGGATT 4335
                                                                                                                             GTTTGGCTATTGCTTCAAFTGGAAAACTCATGTTTGCTCAATTCTCTGATCTTGTCAATG 4275
                                                                                                                                                    GTCTCGCCATTGCTGCAATCGGAAAACTCATGTTCGCTCAATTTTCTGAGCTGGTTAACG 1400
                                                                                             ATTTCTACAACAATGGATTACCATCGAATCTCTCCGGTGGACGTAACCCTAGTTTGGACT 1460
                                                                                                                                                                                                                                                                                                                                                   TTAGAACTTCACCCCAATGGCTTGGTCCTCAAATTGAAGTGATCAGGTTTTCTACCAAGT 4095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TATTTGATGCTAATGTACTTGCGTTGTTGTCGGAAGTGTTATCGGCGATCTTCGCTGAGG
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Conservative
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                                                      TTCCAATTTGTTAG 5129
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AAC61194
                                                 AAC61194 standard; DNA; 4415 BP
                                   12-FEB-2001 (first entry)
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Pea; promoter; plant; prevention; pathogen; infection; ds

Pea PSPAL1 DNA sequence SEQ ID 9.

Pisum sativum

JP2000245463-A

12-SEP-2000

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pea PSPALL gene used in an example to illustrate the use of the promoter of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention relates to movel DNA with promoter activity, comprising the promoter fragments represented by Ancilla6 and Ancilla7. The DNA can be used for the prevention of inferrition of a pathugenic microbe in the roots, leaves and stems of a plant. The present sequence represents the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 11:13, 17pp, Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel DNA with promoter activity, useful for the prevention of a pathogenic microbe from the roots, leaves and stems of a
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(NISB ) JAPAN TOBACCO INC.
(TAKS ) TAKASAGO PERFUMERY CO LTD.
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                                                                                                       CTGGTTTACTAACGGGAAGCCAAATTCAAAAGCTCATGGGAACCTCTGGGGGAAATTCTTA 2778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCGGCCTCTTAACCGGCCGCCCCAACTCCAAAGCCGTTGGCCCCACCGGAGAAGTCCTCA 800
                                       CGGCGCAAAAGGTCCACGAAATGGACCCGTTACAGAAACCAAAACAAGATCGTTATGCTC 1160
                                                                                   GTCANATTGAGGCTGCTACTATTATGGANCACATTTTGGATGGAAGTGCTTATGTCAAAG
                                                                                                                                                               TTATGCAAGGGAAACCTGAGTTTACTGATCATTTGACACATAAATTGAAGCACCATCCTG
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                                                                                                                                                                                                                                                                                        TATTTIGATICCTAATGTACTTGCGTTGTTGTGTGGGAAGTGTTATCGGCGGATCTTCGCTGAGG 980
                                                                                                                                                                                                                                                                                                                                  AAGAAGGTCTTG: ACTTGTTAATGGAACTGCTGTTGGTTCTGGTTTAGCTTCTATTGTTC 2898
                                                                                                                                                                                                                                                                                                                                                                                                                   ATGCAAAAGAAGCTTTTCAGTCAGCTGAAATCAATGATGGTTTTCTTTGAATTGCAACCAA 2838
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                                                                                      GCAAAGGTCAAATTATTIGATCCGTTGTTGGAGTGTGTTTGGAGGGTGGAATGGGGGAACCTC 2240
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                                                                                                                                                                                     TOACCCGAGAAAAGGTGACGTCGCCGGGAGAGGAGTTTCGACAGGGTGTTCACGGCGATGTC 2180
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                                                                                                                                                                                                                                                                                      Query Match 39.8%; Score 970.8; DB 14; Length 4415; Hest Local Similarity 70.0%; Pred. No. 9.4e-165; Matches 1335; Conservative 0; Mismatches 567; Indels 4;
                                                                                                                                                                                                                                 2482 TCAGGTTTTGAATGCTGGAATATTTGGAAATGGAACTGAGTCAAGCCATACACTACCAC 2541
                                                                                                                                                                                                                                                                                                                                                                         The regulatory fragment of the phenyl alanine ammonia lyase gene is capable of artificially accelerating or suppressing the transcription of the structural gene of a plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4338 AATTTCTTTTAATGTCAATGTGAAACTTGTAATTTACTTTTATAAT 4383
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2719 CIGGTTTACTAACGGGAAGGCAAAITCAAAAGCTCAIGGGACCTCIGGGGAAAITCITA 2778
                                                         2602 GAATTAGATTTGAAATCTTGGAAGCTATAACCAAACTCATTAACAACAACGTCACCCCAT 2661
                                                                                                                                                                        2542 ACACAGCAACAAGAGUTGUCATGUTTUTGAGAATQAAQAQACAGTTQTUUAAGGTTATTQAG
                                                                                                                                                                                                                                                                                                                                               Sequence 4415 BP; 1415 A; 725 C; 793 G; 1482 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 2; Page 7-8; 9pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Regulator gene of specified sequence - and phenylalanine ammonia lyase gene of pea with specified sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TAKS ) TAKASAGO PERFUMERY CO LTD
                           741 CCGGCCTCTTAACCGGCCGCCCCAACTCCAAAGCCGTTCGCCCCACCGGAGAAGTCCTCA 800
                                                                         681 GTTTACCCCTCCGTGGAACCATCACCGCTCCGGTGACCTTGTCCCATTATCATACATCG 740
                                                                                                                                          621 GCATCCGATTCGAGATCTTGGAAGCCATCACCAAGTTCCTTAACAACAACATCACCCCTT 680
                                                                                                                                                                                         561 ATTCAGCCACCACGCCATGATCGTCAGAATCAACACCCTCCTCCAGGGTTACTCCG 620
                                                                                                                                                                                                                                                              501 TTAGATTTTTGAACGCCGGAATATTCGGCAATGGAACGGAAACAAGCCACACACTTCCAC 560
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                                                  Antisense CAD gene fragment is inserted into the plant under the control of a promoter, using Aurobacter tumefacters (pref 114464) as a vector. Sequence inhibits lighth biosynthesis in the plant improving digestibility of animal foder, and useful in production
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                            Pisum sativum
                                                                                                                                                                                    07-MAY-1993 (first entry)
                                                                                                                                                                                                                                                                               AAQ33019 standard; cDNA; 1707
                                                                                                                                                                                                                                                                                                                                                                                                2906 CTGTGTTATGATTTGCGTTTTATTTTTTTTTGTAGAT 2939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2178 TGTGCAAAGGTCAAATTATTGATCCGTTGTTGGAGTGTCTTGGAGGGTGGAATGGGGAAC
                                                                                           Phenylalanine ammonia lyase; phenyl propanoid isoflavonoid; plant;
                                                                                                                                        Pisium sativum L PAL gene.
                                                                                                                                                                                                                                      AAQ33019;
                                                                                                                                                                                                                                                                                                                                                                                                                                         2298 CTTTTTTTTTTTTTTTTTAAATTTTATTTGCAT 2331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2846 CCATCCCAATATAGTGTTTAATGTAATATTGTTTCACAATAACTAGCCAGGAAGATTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2238 CTCTTCCAATATGTTAGGAAAGTGAGTGTGAAACCGTTTGAATTGTAATTTCTAATATTCT 2297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2726 TGCTCACCGGCGAAAAAGCTCTCTCTCCAGATGAGGAATTTGAAAAGGTTTATACAGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2666 TCAAGGAGTGATATCCACTGTACAAATTTGTGAGGAAGAAGTTAAGGATAACGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1998 AAGAAGTTGAAGGTGTTAGAATCGCTTATGAGAATGATACATTGTCGATTCCAAACAGGA 2057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1818 GTGAATACGTCTTCGCTTACATCGACGACGTTTGCAGCGGCACATACCCCATTAATGCAGA 1877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1758 TCAACGGCGAGCTCCACCGTCGAGATTCTGCGAGAAAGATCTCCTCCGTGTTGTTGATC 1817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1698 TGAAATCGACAGTGAAGAACACCGTAAGCCAAGTCGCGAAAAAAGGTCCTCACCATGGGCG 1757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2126 TAGCANATCCAGTANCCAGCCATGTGCANATACTGAGCAGCACCAACCAAGATGTGAATT 2185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2786 TGTGTCAAGCAAAGATAATTGATCCAATTCTGGAATGTCTAGAAGATTGGAACGGGGTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2546 GTTTGTTGGTTTTTGAGAAGATTGGAGCTTTTGAGGATGAGTTGAAGTCTCTCTTGCCAA 2605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2486 AACTAAAGCAGGTACTTTATGAGCAAGCACATACCAGTGTCATTAATGACAAGAATGTGA 2545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1878 AGCTCCGACAGGTTCTGGTCGACCACGCTCTAAACAACGGCGAAAACGGAGAAGAACACTA 1937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2426 GAGAATATGTATTTTCATACATTGATGATCCCTTAAATGTAAGGTACCCATTGATGCCAA 2485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2366 ACAAAGAAGAAACTAACCCATTTCGATTCAGTGAGGAAGAACTGCTTAAAGTGGTGGATA 2425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2306 TCAAGAACACTGTCAAGAATACTGTGAGCAGAGTTGCACTGAAAAACATTAACTACTGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                        1336 CACCCGTCTCGCCATTGCTGCAATCGGAAAACTCATGTTCGCTCAATTTTCTGAGCTGGT 1395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence is that of the phenylalanine ammonia lyase (PAL) gene from Pisum sativum L. The gene may be used to produce PAL recombinantly. Plants contg. the PAL gene can contain a large amt of phenyl propanoid isoflavonoid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1036
                                                                                                                                    1276 AAACAAAGCTTTACACGGTGGTAACTTCCAAGGAACCCCAATCGGAGTTTCCATGGACAA 1335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 8; 9pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New phenylalanine ammonia lyase gene from Pisum sativum L. - plasmid contg. gene, and E. coli transformed with plasmid, for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JP04330285-A
                                                                                                                                                                                                                                                                                                                                                                                                              1096 CAAGGCGGCGCAAAAGGTCCACGAAATGGACCCGTTACAGAAACCAAAACAAGATCGTTA 1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1707 BP; 496 A; 345 C; 377 G; 489 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   See also AAQ31985.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                prepn. of lyase.
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                                                                                                                                                                                 481 CAAGTCAATTGAGAGAGAGATTAACTCCGTGAATGACAACCCTCTTATTGATGTTTCAAG
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                                                                                                                                                                                                              CAAAATGATCGAGAGGGAAATCAATTCCGTCAACGACAACCCATTGATCGACGTTTCCAG 1275
                                                                                                                                                                                                                                                                                                                                                                 CCCTGGTCAAATCGAGGCGGCGAGCATCATGGAGTATATTTTGGACGGAGGCGATTACGT 1095
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                                                                                        GAACAAGGCATTGCATGGTGGTAATTTCCAAGGAACCCCAATTGGAGTCTCCATGGACAA
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                                                                                                                                                                                                                                                                                                                   TGCTCTCCGTACATCTCCCCAATGGCTCGGACCTCAAATCGAAGTAATCCGATCATCAAC 1215
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Plant; lignin; lignin biosynthetic pathway; Eucalyptus grandis;
                                                                                                                                                                 AAA68152 standard; DNA; 1455 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1261 AAAGGAGGTTGAAAAGTACAAGGGCTGCTTATGAGAGTGGGAAAGCTGCAATTCCAAACAA 1320
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                                         Eucalyptus grandis PAL nucleotide sequence SEQ ID NO:245
                                                                                                                              AAA68152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1081 CAGGGAGTATGTATTTTCCTACATAGATGACCCATACAGTGGTACATACCCCACTGATGCA 1140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTTTTTGACCGGAGAAAAGGTGACGTCGCCGGGGAGAGGAGCACTTCGACAGGTGTTGACGGC 2175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TAACACCTCCATCTTCCAAAAGATCGCTACCTTCGAAGAAGAATTGAAAGTCCTGTTACC 1995
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                                                                                                                                                                                                                                                                                                                                                         AATTATIGCCAGGGCAAAATTAFTGATCCTCTTCTCGAATGCCTTGGAGAGTGGAATGGAGC 1500
                                                                                                                                                                                                                                                                                                                                                                                              GATGTGCAAAGGTCAAATTATTTGATTCGGTTGTTTGGAGTGTCTTGGAGGGTGGAATGGGGA 2235
                                                                                                                                                                                                                                                                                                                                                                                                                                       GTTGCTAACTGGAGAAAAGGTGAAGTCACCAGGTGAAGAGTTTTGACAAGTTATTCACAGC 1440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GATAAAAGAATIGCAGATICTTIACCCACTICTIACAAGTTTTGTIGAGAGAGGAGTTTIGGGGCACTIGG 1380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAAAGAAGTTGAAGGTGTTAGAATCGCTTATGAGAATGATACATTGTCCATTCCAAACAG 2055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCGTGAATACGTCTTCGCTTACATCGACGACGTTTGCAGCGGCACATACCCCATTAATGCA 1875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTTGAAAAGCTCGGTCAAGACACTGTGAGTCAAGTTTCCCAAGAGGACTCTTACCACAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATGAAATCGACAGTGAAGACACCGTAAGCCCAAGTCGCGAAAAAAGGTCCTCACCATGGG 1755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GICTIFCCACGIFCIFIGATICGGACTTTGCCCAAGCAATTGACTTCAGGCATTTGGAGGAGAA 960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTCGTCGACATACTTAGTCGCTCTATGCCAATCCATCGATTTACGCCATTTGGAAGAGAA 1695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTCTTTGGATTTGATTTCAGCTAGGAAGACAAATGAATCTATTGAGATCCTTAAGCTCAT 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTCTCTCGGATTAATTTCAGCGAGGAAAACCGCAGAAGCAGTCGACATCTTAAAACTCAT 1635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCTGGCAAATCCAGTAACAAGCCATGTCCAAAGTGCTGAGCAACACAACCAAGATGTGAA 840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGACTACGGGTTCAAAAGGTGGAGAATCGCCATGGCTTCTTACTGTTCTGAGCTTCAGTT 1515
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                                                                                     (first entry)
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Qy Db

410 AAAGGAACTGATAGTTATGGTGTCACCACCGGCTTTCGGCGCGCCACCTCTCACCGGAGAACT 469

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254 GADOUACTGAACTGGGGGGGGGGGGAAGCAGCCTCACAGGGAGCCACCTCGACGAGGTG 313

170 GATCCATTGAACTGGGGAGTTGCAGCGGAGGCGTTGACCGGAAGTCACCTTGATGAGGTG

290 HTTPTT/MHSTHER GEHEATCHE ANSCTHET TAATGACARTEN AN THE GARDET BEARETTE 349
291 HTTPTT/MHSTHER GEHEATCHE ANSCTHET TAATGACARTEN AND THE GEHEATCHET THE TENTE THE TENT

350 TCGGAAGCCGCGAGGGCTTGGAGTTAAGGCCGAGTAGTGATTGGGTTFATTGGAGAGGATGAAT

Matches

Conservative

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Mismatches 290, Indeis

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Query Match
                                                                                                                                                                                    coumerate CoA ligase, cytochrome P450 LXXIA, diphenol oxidase, flavanol glucosyl transferase, flavenoid hydroxylase, and isoflavone reductase, which are involved in the lignin biosynthetic pathway. The polynucleotides can be used for modulating lignin content, lignin composition and the structure of a plant, especially eucalyptus and pine species, and for modifying the activity of an enzyme involved in lignin biosynthetic pathway, and for producing a plant having altered lignin content, composition and structure. They can be used for designing probes and primers useful for detecting similar DNA and RNA sequences in any
                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes isolated polynucleotides and proteins encoding and representing the enzymes cinnamate 4-hydroxylase (C4H), coumarate 3-hydroxylase (C3H), phenolase (PNL), O-methyl transferase (OMT), cinnamyl alcohol dehydrogenase (CAD), cinnamoyl-CoA reductase (CCR), phenylalanine ammonia-lyase (PAL), 4-coumarate:CoA ligase (4CL), coniferol glucosyl transferase (CGT), coniferin beta-glucosidase (CBG),
                                                                                                                            organism and for PCR amplification. The lianin content can be efficiently modified using the polynucleotides. AAAb7908 to AAAb8201 and AAB16341 to AAB16449 represent polynucleotide and protein sequences used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel polynuclectide encoding enzymes involved in lignin-biosynthetic pathway useful for producing transgenic plants especially eucalyptus and pine species having altered lignin content, composition and
                                                              Sequence 1455 BP; 307 A; 442 C, 431 G, 275 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                    laccase, peroxidase, ferulate-5-hydroxylase (F5H), alpha:amylase, caffeic acid methyl transferase, caffeoyl CoA methyl transferase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 131-132, 213pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-OCT-1998;
14-JUL-1999;
                                                                                                    exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bloksberg LN, Havukkala IJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GENE-) GENESIS RES & DEV CORP LID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-0CT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eucalyptus grandis
    / Match 29.4%;
Local Similarity 75.3%;
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Score 719; DB 21
Pred No le-119;
                      DB 21;
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RESULT 14
ABN87223
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ABN87223;
                                                                                                                                                                                         1445 ATGTTCGCGCA 1455
                                                  ABN87223 standard; cDNA; 1503 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1145 CACATTTTGGATGGAAGCGCTTACGTGAAGGCTGCTAAAAAGTTTGCACGAGATGGATCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1070 TATATTTTGGACGGAAGCGATTACGTCAAGGCGGCGCAAAAGGTCCACGAAATGGACCCG
                                                                                                                                                                                                                                        ATGTTCGCTCA 1380
                                                                                                                                                                                                                                                                                                                                                                                                                                                        GACAACCCATTGATCGACGTTTCCAGAAACAAAGCTTTACACGGTGGTAACTTCCAAGGA 1309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAGATTGAGGTGATCCGAGCGGCAACCAAGATGATTGAGAGGGAAATCAATTCGGTCAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAAATCGAAGTAATCCGATCATCAACCAAAATGATCGAGAGGGAAATCAATTCCGTCAAC 1249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTCCAGAAGCCAAAGCAGGACAGGTACGCTCTCAGGACTTCTCCCCCAGTGGCTAGGGCCC 1264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCCGAGGTCCTGTCAGCGATCTTCGCAGAGGTGATGCAGGGGAAGCCGGAGTTCACAGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTTGAAGGTGGGTTCTTCGAGTTACAGCCGAAAGAAGGGCTAGCACTTGTTAACGGCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAGGCCGTCGGGCCTGATGGGAAGTCCCTGGACGCTGTCGAGGCCTTCCGGCTCGCCGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AACGGCACGGAGTCGTGCCACACCCTGCCTCAATCCTCCACCCGAGCCGCCATGCTCGTC
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                                                                                                                                                                                                                                                                                                                                             ACCCCAATCGGAGTTTCCATGGACAACACCCCGTCTCGCCATTGCTGCAATCGGAAAACTC
                                                                                                                                                                                                                                                                                                                                                                                                        GACAACCCGCTGATCGATGTCGCGAGGAACAAGGCCCTGCACGGTGGGAACTTCCAGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCAGTCGGGTCTGGCCTGGCTTCCATCGTCCTCTTCGAGGCCAACATACTCGCGGTCCTG 1024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCCGTGGGGTCCGGGATGGCTTCCATGGTTCTATTTGATGCTAATGTACTTGCGTTGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAAGCCGTTGGCCCCACCGGAGAAGTCCTCAATGCCGAAAAGGCCCTTCGCTGCAGCCGGA 829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCCGGTGACCTTGTCCCATTATCATACATCGCCGGCCTCTTAACCGGCCGCCCCAACTCC
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                                                                                                                                                                                                                                                                                              ACCCCGATTGGTGTCTCCATGGACAACACTCGCCTGGCGGTTGCGTCCATAGGGAAGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCGGAAGTGTTATCGGCGATCTTCGCTGAGGTTATGCAAGGGAAGCCGGAGTTTACCGAT 1009
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Claim 11; Fig 62; 436pp; English.

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Novel nucleic acid encoding lignification and cellulase enzymes or their related enzymes useful for modifying lignin biosynthesis and cellulose degradation in plants to manipulate plant cell wall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             caffeoy1-CoA 3-0-methyltransferase; cinnamyl alcohol dehydrogenase; CAD;
caffeic acid 0-methyltransferase; OMT; cinnamate-4-hydroxylase; C4H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F5H; CELL; phenylalanine ammonia lyase; PAL; 4-coumarate:CoA ligase; 4CL; ryegrass; fescue species; molecular genetic marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lolium perenne LpPALa nucleotide sequence SEQ ID NO:140.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-JUL-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                  Spangenberg G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-SEP-2000; 2000AU-0000419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-SEP-2001; 2001WO-AU01221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200226994-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lolium perenne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cellulase; enzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lolium perenne; perennial ryegrass; plant; cell wall; lignification;
                                                                                                                                                                                                                                                                                                                                                                                                                                         (AGRE-) AGRESEARCH LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cinnamoyl-CoA reductase; CCR; peroxidase; PER; ferulate-5-hydroxylase;
                                                                                                                                                                                                                                                                                                                                                                                             2002-444025/47
                                                                                                                                                                                                                                                                                                                                                                                    ABB78982
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGRIC VICTORIA SERVICES PTY LTD
                                                                                                                                                                                                                                                                                                                                                                                                                   Sawbridge TI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lignin biosynthesis; cellulose degradation; CCOAMT;
                                                                                                                                                                                                                                                                                                                                                                                                                   Ong EK, Emmerling
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mechanical stress tolerance, disease resistance, insect pest resistance, plant stature, leaf and stem colour. The present sequence represents a Lolium perenne (perennial ryegrass) nucleotide sequence from the present hybridisation probes to screen libraries from the desired plant. Short segments of (I) or its fragment are useful in amplification protocols to amplify longer nucleic acids or its fragments encoding homologous genes from DNA or RNA. (I) or its fragments are useful as molecular genetic markers for quantitative trait loci (QTL) tagging, QTL mapping, DNA fingerprinting, and in marker assisted selection, particularly in ryegrass and fescues, and in forage and turf grass improvement, e.g. tagging QTLs for herbage quality traits, dry matter digestibility, ryegrass (Lolium perenne) or fescue species. (1), its nucleotide sequence information and/or single nucleotide polymorphisms is useful as a molecular genetic marker. (I) can be used for modifying lighin biosynthesis and/or cellulose degradation in a plant to manipulate cell walls. (I) or its fragments are useful for isolating cDNAs and genes encoding homologous proteins from the same or other plant species, as The present invention describes a nucleic acid (1) or its fragment encoding caffeoyl-CoA 3-O-methyltransferase (CCOAMT), cinnamyl alcohol dehydrogenase (CDD), caffeic acid O-methyltransferase (OMT), cinnamate-4-hydroxylase (C4H), cinnamoyl-CoA reductase (CCR), peroxidase (PER), cellulase (CELL), ferulate-5-hydroxylase (F5H), phenylalanine ammonia lyase (PAL) or 4-coumarate:CoA ligase (4CL) from perennial invention.

Sequence 1503 BP; 339 A; 427 C; 407 G; 310 T; 20 other;

Matches 897 GGTCCGGGATGGCTTCCATGGTTCTATTTGATGCTAATGTACTTGCGTTGTTGTCGGAAG 6 GGCTCCGGCTCCATGGTGCTCTTCGAGGCCAACATCCTTAGCCTCCTTGCCGAGG Similarity Conservative 27.4%; Score 668.8; 65.8%; Pred. No. 9.1 16; Mismatches 9.8e-111; DB 24; 475; Indels Length 1503; 0; 65

0;

QΥ 957 TGTTATCGGCGATCTTCGCTGAGGTTATGCAAGGGAAGCCGGAGTTTACCGATCACTTGA 1016 

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1017
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CCGCCGAGGCAGCAAAAACCGCAFCACCGAAAAGACGGTCATACCCGCTGTATCGCTTCGTGC 1205
                                                                                                                                       CATTGTCGATTCCAAACAGGATTAAAGCTTGCAGATCGTACCCGTTGTATAGGTTTGTAA 2096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTGAGGCTCACCGGCATCTGCACACCTCAGTGTTCGGCCAÁGCTCGGCGCATTCGÁGCÁGG
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                                                                                                                                                                                                                                                                              AGCTCCCTGCGCTGCTTCCAAGGGAGGTCGAGTCAGCCGGTGYGCGCTGGGAGAATGGCA ] 1145
                                                                                                                                                                                                                                                                                                                                                                                                      AATTGAAAGTCCTGTTACCGAAAGAAGTTGAAGGTGTTAGAATCGCTTATGAGAATGATA 2036
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Pinus radiata PAL nucleotide sequence SEQ ID NO:247
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                                                                                                                                                                                                                                                                                                                                                                                                                Pinus radiata; Monterey pine; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAA68154;
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                                                                                                                                                                                                                                                                              (FLET-) FLETCHER CHALLENGE FORESTS LTD
                                                                                                                                                                                                                                                                                       (GENE-) GENESIS RES & DEV CORP LID
                                                                                                                                                                                                                                                                                                          14-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                           Havukkala IJ;
                                                                                                                                                                                                                                                                                                                                                                                                                       lignin biosynthetic pathway, Eucalyptus grandis;
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polynowheatides can be used for modulating lighth content, lighth composition and the structure of a plant, especially eucalyptus and pine species, and for modifying the activity of an enzyme involved in lighth biosynthetic pathway, and for producing a plant having altered lighth content, composition and structure. They can be used for designing probes and primers useful for detecting similar DNA and RNA sequences in any (CCR), phenylalanine ammonia-lyase (FAL), 4 coumaraté:COA liqase (4CL), coniferol qlucosyl transferase (CGF), coniferon beta glucosidase (CGF), laccase, peroxidase, ferulate-5-hydroxylase (FSH), alpha-amylase, caffere acid methyl transferase, caffeoyl FOA methyl transferase, coumerate CoA ligase, cytochrome P450 lixiA, diphenol oxidase, flavanol glucosyl transferase, tlavenoid hydroxylase, and isoliavone reductase, which are involved in the lignin biosynthetic pathway. The encoding and representing the enzymes cinnamate 4-hydroxyiase (C4H), commarate 3-hydroxylase (C3H), phenolase (PNL), 0-methyl transferase (OMT), cinnamyl alcohol dehydrogenase (CAD), cinnamoyl-CoA reductase Novel polynucleotide encoding enzymes involved in lignin-biosynthetic pathway useful for producing transgenic plants especially eucalyptus and pine species having altered lignin content, composition and The present invention describes isolated polynucleotides and proteins Claim 1; Page 132-133; 213pp; English

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organism and for PCR amplification. The light content can be efficiently modified using the polynucleotides. AAA67908 to \DeltaAA68201 and AAB16341 to AAB16449 represent polynucleotide and protein sequences used in the exemplification of the present invention.
1614 CAGTOGACATOTTAAAACTCATGTCGTCGACATACTTAGTCGCTCTATGCCAATCCATCG 1673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1314 CAATCGGAGTTTCCATGGACACACCCGTCTCGCCATTGCTGCAATCGGAAAACTCATGT 1373
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1520 BP; 389 A; 356 C; 376 G; 399 T; 0 other;
                                                                                                                                                                                                                                   1554 AACAACAATAAAGAAGTTAATTCTCTCGGATTAATTTCAGCGAGGAAAAACGGCAGAAG 1613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1434 CCGGTGGACGTAACCCTAGTTTGGACTACGGGTTCAAAGGTGGAGAAATCGCCATGGCTT 1493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1254 ACCCATTGATCGACGTTTCCAGAAACAAAGCTTTACACGGTGGTAACTTCCAAGGAACCC 1313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          714 GTGACCTTGTCCCATTATCATACATUGUCGGCCTCTTAACCGGCCGCCCCAACTCCAAAG 773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 TCAGATCCAGAGATGGAATTGAAATGAGCGGAGCCGAAGCGCTCAAGAAAGTGGGCCTGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
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                                                                                                                                       AACAGCATAACCAGGATGTCAATTCTCTGGGTCTCGTTTCAGCTAGAAAATCTGCCGAGG 896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTGGTGGGCCTAATCCCAGCCTGGATTATGGACTGAAAGGGGCCGAGATCGCTATGGCTT 776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCGCTCAATTCTCAGAGCTTGTGAATGATTACTACAATGGAGGCTTGCCTTCGAATCTGA 716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCGCTCAATTTTCTGAGCTGGTTAACGATTTCTACAACAATGGATTACCATCGAATCTCT 1433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTATTGGTGTTTCCATGGATAATCTTCGTCTGTCAATTTCAGCAATTGGGAAATTGATGT 656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATCCAGTAATTGATGTTGCCAGAGACAAAGCTCTACATGGAGGGAATTTCCAGGGCACAC 596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGGAGATTATCAGATCTGCAACTCACATGATTGAGCGGGAAATCAATTCTGTGAATGACA 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGAAACCAAAACAAGATCGTTATGCTCTCCGTACATCTCCCCAATGGCTCGGACCTCAAA 1193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCTTGGACGGGAG-TCTTATATGAAACACGCTGCTAAGCTCCATGAGATGAATCCTCTGC 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAACTCACAAGCTGAAGCACCATCCTGGCCAAATGGAAGCTGCAGCGATCATGGAGTATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAGTAATCTCTGCCATGTTCTGGGGAGGTTATGAATGGGAAGCCTGAGTTTACAGATCCAT 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAGGTGGGTTCTTCGAGTTACAGCCGAAAGAAGGGCTAGCACTTGTTAACGGCACCGCCG 893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCGTTGGCCCCACCGGAGAAGTCCTCAATGCCGAAAAGGCCTTCGCTGCAGCCGGAGTTG 833
                                                                                                                                                                                                                                                                                                                      CTTACACTTCTGAGCTTCTTTACCTGGCAAATCCTGTCACCAGCCATGTACAGAGCGCCC 836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGAAGCCAAAGCAGGATCGCTATGCGCTTCGCACTTCGCCTCAGTGGCTCGGCCCTCAGG 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAGTGTTATCGGCGATCTTCGCTGAGGTTATGCAAGGGAAGCCGGAGTTTACCGATCACT 1013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA---AAGCCCTTTGAATTGCAGCCTAAAGAAGGTCTGGCCATTGTCAATGGCACTTCAG 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGGGAGCACTGGCTTCCATTGTGTGTTCGATGCCAATGTTCTTGCTCTGCTCTCTG 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 6.2e-106;
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1377 TGAGAAACCAGCTCGGTA 1394
                                                             2094 TAAGGGAGGAGCTCGGCA 2111
                                                                                                                        1317 GGACCAGCCCTCTGCCCAACAGGATCCAGGAATGCAGGTCTTATCCTCTCTATGAATTTG 1376
                                                                                                                                                        2034 ATACATTGTCGAGTTCCAAACAGGATTAAAGCTTGCAGATCGTACCCGTTGTATAGGTTTG
                                                                                                                                                                                                                                             1257 CCGAGCTGAAGGCACAGCTTGAACCGCAAGTTAGTCTGGCCAGAGAAAGTTATGACAAAG 1316
                                                                                                                                                                                                                                                                                                              1974 AAGAATTGAAAAGTCCTGTTACCGAAAGAAGTTGAAGGTGTTAGAAATCGCTTATGAGAATG 2033
                                                                                                                                                                                                                                                                                                                                                                                                                                   1914 ACGGCGAAACGGAGAAGAACACTAACACCTCCATCTTCCAAAAGATCGCTACCTTCGAAG 1973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1137 ATGCCAGCTACCCATTGACTCAGAAACTGAGAAACATCCTGGTGGAACATGCCTTCAAGA 1196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1854 GCGGCACATACCCATTAATGCAGAAGCTCCGACAGGTTCTGGTCGACCACGCTCTAAACA 1913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1077 AGGATTTGCTCCAGGTAGTGGATAACGAACATGTTTTCTCTTACATTGACGATCCGTGCA 1136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1794 AAGATCTCCTCCGTGTTGTTGATCGTGAATACGTCTTCGCTTACATCGACGACGTTTGCA 1853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1017 CCAAGAAAACCCTGAGCACAGGGCTCAACGGGGAGCTTTTGCCAGGCCGTTTCTGCGAAA 1076
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1674 ATTTACGCCATTTGGAAGAACATGAAATCGACAGTGAAGAACACCGTAAGCCAAGTCG 1733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       957 ATTTAAGGCATCTGGAGGAAAACATGCTGGCCACTGTGAAGCAGATTGTTTCTCAGGTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            897 COATCGATATTCTGAAGCTGATGCTCTCCACATACCTGACAGCTCTGTGCCAGGCTGTGG
                                                                                                                                                                                                                                                                                                                                                                      ACCCAGAAGGTGAGAAGGATCCCAACACTTCCATTTTCAATAAGATTCCTGTGTTTGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1016
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Search completed: March 28, 2003, 21:56:09 Job time: 556 secs

GenCote version 5  $^{\circ}$   $^{\circ}$   $^{\circ}$   $^{\circ}$  4_F5_4578 Copyright (c) 1993 - 2003 Compugen Ltd

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OM protein - protein search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Perfect score.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                  A_Graceseq_101002.*

1. /SIDS2/rejidata/jerneseq/armesergr-embl/AA1980 :A1.*

2. /SIDS2/gegidata/geneseq/genesedp_embl/AA1981.LA1.*

3. /SIDS2/gegidata/genesedp_embl/AA1982.DAT.*

3. /SIDS2/gegidata/genesedp_embl/AA1984.DAT.*

5. /SIDS2/gegidata/genesedp_embl/AA1984.DAT.*

6. /SIDS2/gegidata/genesedp_embl/AA1985.DAT.*

6. /SIDS2/gegidata/genesedp_embl/AA1985.DAT.*

8. /SIDS2/gegidata/genesedp_embl/AA1987.DAT.*

7. /SIDS2/gegidata/genesedp_embl/AA1987.DAT.*

8. /SIDS2/gegidata/genesedp_embl/AA1987.DAT.*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                March 28, 2003, 23.41.56 , Search time 67 Seconds (without alignments) 1414.048 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          908470 seqs, 133250620 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BLOSHM62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                            /SIDS2/qcqdata/qeneseq/qeneseqp-embl/AA1988.DAT:*
                                                                                   /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1997.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1998.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*
                                                                                                                                                                                                            /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1993.I/AT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1994.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT:*
/SIDS2/qcqdata/qeneseq/geneseqp+embl/AA2002.DAT.*
                            /SIDS2/gcqdata/geneseq/geneseqp-emb1/AA2000_DAT-*/SIDS2/gcqdata/geneseq/geneseqp-emb1/AA2001_DAT.*
                                                                                                                                                                                                                                                                                                                                     /SIDS2/gcgdata/geneseq/geneseqp·embl/AA1991.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                  /SIDS2/qcqdata/geneseq/geneseqp-emb1/AA1989.DAT:*
                                                                                                                                                                                  /SIDS2/qcqdata/qeneseq/qeneseqp-embl/AA1996 DAT:*
                                                                                                                                                                                                                                                                                                     /STDS2/gogdata/gotosog/gotosogp=emb1/AA1992.DAL:*
                                                                                                                                                                                                                                                                                                                                                                  /SIDS2/qcqdata/geneseq/geneseqp-emb1/AA1990.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . ППРИЛЕГЬЗЭМИЗЕРИЛЕ 711
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

## SUMMARIE

Result No.	Score	Query Match	Query Match Length DB		(1)	Description
-	3644	100.0	711	77	AAU97130	Lettuce LsPAL1 enz
NJ	3294	90.4	712	ر برا	AAU97131	
ω.	3059.5	84.0	777	14	AAR30077	
4	3045.5	83.6	725	<u>د.</u>	AAC36709	Arabidopsis thalia
S)	3044.5	83.5	709	21	AAC36710	Arabidopsis thalia
6	3041.5	83 5	869	21	VVC36211	Arabidopsis thalia
7	3004	82.4	711	21	AAG54103	Arabidopsis thalia
æ	3004	82.4	717	21	AAG54102	Arabidopsis thalia
4	2951	81.0	681	<u>ب</u>	AAC54104	Arabidopsis thalia
10	2907.5	79.8	736	<u>၊</u>	AAC53399	Arabidopsis thalia

45	44	43	4.	4	40	39	86	37	36	35	ب 4-	w w	ري دع	لدا در	30	29	t2 80	27	PU ON	25	1,4	2.3	t.3 (1)	21	20	19	18	17		15	14	13	7.	1.1
971.5	3.046	984.5	344.5	2 X 4 X 5	987.5	987.5	988	990.5	990.5		991.5	٠	991.5				994.5				994.5		305.5	1025	1337	1345	1475	1709	1752	1779	1799	1892	1548	2807
26.7	14	27.0	27.0	27 1	27.1	27.1	27.1						٠		27.2		27.3	27 3	27.4	27 7	27.3	27.3	27.3	28.1	36.7	36.9	40.5	46.9	4 tb . }	48.8	9.	51.9	72.7	77.0
713	7 <u>î</u> h	716	716	7 ! 6.	716	716	686	716	716	716	716	716	716	716	716	716	716	716	716	716	716	71b	716	720	304	412	489	386	346	495	424	423	5 A B	699
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ABB07692	AAE20558	ME20711	AAE20551	AAF20663	AAE#U656	AAR70682	AAE20657	AAE20662	AAE20660	AAE16390	AAE20668	AAE20667	AAE20659	AAE20654	AAE20665	AA1:95783	AAE16384	ABR07693	AAE20653	AAP81099	AAP83141	AAP80513	AAE20664	ABB07690	AAU12066	AAB16404	ABB78983	AAG21949	AAC21948	ABB78982	AAB16402	AAG21947	AAG53401	AAG53400
cilaq	a	R. glutinis phenyl			R. glatinis phenyl	Stabilised phenyla	Rhodotorula glutin	Rhodotorula glutin	Rhodotorula glutin	a:	ů.	R. glutinis phenyl	Rhodotorula glutin		R. glutinis phenyl	L-phenylalanine am	Rhodotorula glutin	R. toruloides PAL		Sequence of Rhodos	Sequence of L-phon		R. glutinis phonyl	R. graminis PAL po	Protein encoded by	Pinus radiata PAL	=		Arabidopsis thalia	Lolium perenne LpP	ú			Arabidopsis thalia

## ALIGNMENTS

RESULT 1 AAU97130

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ΞX
Novel polynucleotide useful in preparing plant expression constructs to modify the response of a plant cell to wounding, damage or other injury
                                                                                                                                                                                                                                                                                                                                                                                  13-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU97130 standard; Protein; 711 AA
                                            N-PSDB; ABK50679.
                                                          WFI; 2002-435152/46.
                                                                                      Saltveit M, Campos R, Nonogaki H,
                                                                                                                                                26-SEP-2000; 200008-235956P
                                                                                                                                                                                                          04-APR-2002.
                                                                                                                                                                                                                                      MO200226028-A2
                                                                                                                                                                                                                                                                  Lactuca sativa
                                                                                                                                                                                                                                                                                                         Lettuse; phenylalanine ammonia-lyase; plant wounding; plant damage; plant browning; vegetable crop; plant; LSPAL1;
                                                                                                                                                                                                                                                                                                                                                      Lettuce LsPALl enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                  AAU97130;
                                                                                                                    (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                           26-SEP-2001; 2001WO-US30192.
                                                                                        Suslow T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Fig 6; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     from disease causing organisms or from plant pests
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 LNNNITPCLPLRGTITASGDLYPLSYIAGLL/TGRPNSKAVGPTGEVLNAEKAFAAAGVEG
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                                                                                               EELGRGFLTGEKVTSPGEEFDRVFTAMCKGQIIDPLLECLGGWNGEPLPIC 711
                                                                                                                                                                                                                                                    KVLTMGVNGELHPSRFCEKDLLRVVDRFYVFAYIDDVCSG1YPLMQK1.KQVLVUHALNNG
                                                                                                                                                                                                                                                                                                                                                                                                                                         QFSELVNDFYNNGLPSNLSGGRNPSLDYGFKGGEIAMASYCSELQFLANPVTNHVQSAEQ 480
                                                         EELGRGFLTGEKVTSPGEEFDRVFTAMCKGQIIDPLLECLGGWNGEPLPIC
                                                                                                                                                                                      ETEKNTNTSIFQKIATFEEELKVLLPKEVEGVRIAYENDTLSIPNRIKACRSYPLYRFVR 660
                                                                                                                                                                                                                                                                                                                HNQDVNSLGLISARKTAEAVDILKLMSSTYLVALCQSIDLRHLEENMKSTVKNTVSQVAK
                                                                                                                                                                                                                                                                                                                                                      HNQDVNSLGLISARKTAEAVDILKLMSSTYLVALCQSIDLRHLEENMKSTVKNTVSQVAK 540
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                                                                                                                                            ETEKNTNTSIFQKTATFEEELKVLLPKEVEGVRIAYENDTLSIPNRIKACKSYPLYRFVR
                                                                                                                                                                                                                              KVLTMGVNGELHPSRFCEKDLLRVVDREYVFAYIDDVCSGTYPLMQKLRQVLVDHALNNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     \tt HKLKHHPGQIEAAAIMEYILDGSDYVKAAQKVHEMDPLQKFKQDRYALKTSFQWLGPQIE
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Pred. No. 2.3e-283;
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AAU97131

AAU97131 standard; Protein; 712 AA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel polynucleotide useful in preparing plant expression constructs to modify the response of a plant cell to wounding, damage or other injury from disease causing organisms or from plant pests \,\cdot\,
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to the isolation of novel lettuce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 2; Fig 8; 46pp; English.
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                241 GFFELQPKEGLALVNGTAVGSGMASMVLFDANVLALLSEVLSAIFAEVMQGKPEFTDHLT
                                                    185 INHNVTPFLPLRGTITASGDLVPLSYIAGLL/TGRANSKAVGPTGEVLNAEKAFAEAGVEG
                                                                                                                                              121 GALQKEL1RFLNAG1FGNGTETSHTLPHSATRAAMIVRINTLLOGYSG1RFE1LEA1TKF 180
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                                                                                        LNNNITPCLPLRGTITASGDLVPLSYIAGLLTGPPNSKAVGPTGEVLNAEKAFAANGVEG
                                                                                                                           GALQKELIRFLNAGIFGNGTESTHTLPHSATRAAMLVRINTLLQGYSGIRFEILEAITKF
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2002-435152/46.
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                                                                                                                                                                                                                                                                                                                                                            90.4%; Score 3294; DB 23; 90.7%; Pred. No. 2.8e-255;
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Query Match
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                                                                    The sequence is that of phenylalanine ammonia lyase (PAL) from Pisum sativum L. The gene encoding PAL may be used to produce PAL recombinantly. Plants contg. the PAL gene can
                                                                                                                                                                           New phenylalanine ammonia lyase gene from Pisum sativum Laplasmid contg. gene, and E. coli transformed with plasmid,
                                                                                                                                                                                                                            N-PSDB; AAQ31985.
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                              Sequence
                                                                                                                                 Disclosure; Page 7; 9pp; Japanese.
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Hest Local Similarity 83.8%; Pred. No. 2.1e-Matches 594, Conservative 57; Mismatches
                                                                                                                                                                                        hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                                                                  Protein identification; signal transduction pathway; metabolic pathway;
                                                                                                                                                                                                                                                            Arabidopsis thaliana protein fragment Sky ID No: 45026
                                                                                                                                                                                                                                                                                                          18-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                              AAG36709 standard; Protein; 725
                                                                                                                                Arabidopsis thaliana
                                                                                                                                                                          termination sequence.
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57; Mismatches 51;
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                            Arabidopsis thaliana
                                                                                  termination sequence.
                                                                                                     hybridisation assay; genetic mapping; gene expression control; promoter,
                                                                                                                                  Protein identification; signal transduction pathway, metabolic pathway;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DFYNNGLPSNI.SGGKNFSLDYGFKGGEIAMASYCSELWFIANFYINHVUSAEQHNQDVNS 487
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                                                                                                                                                                                                                                                                                                                                                TTGINGELHPSRFCEKDLLKVVDREQVFTYVDDPCSATYPLMQRLRQVIVDHALSNGETE
                                                                                                                                                                                                                                                                                                                                                                            TMGVNGELHPSRFCEKDLLRVVDPEYVFAYIDDVCSGTYPLMQKLRQVLVDHALNNGETE
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ELVNDFYNNGLPSNLTASSNPSLDYGFKGAEIAMASYCSELQYLANPVTSHVQSAEQHNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ELVNDFYNNGLPSNLSGGRNPSLDYGFKGGEIAMASYCSELQFLANPVTNHVQSAEQHNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KHHPGQIEAAAIMEYILDGSDYVKAAQKVHEMDPLQKPKQDRYALRTSPQWLGPQIEVIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DLQPKEGLALVNGTAVGSGMASMVLFEANVQAVLAEVLSAIFAEVMSGKPEFTDHLTHRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  {\tt NISPSLPLRGTITASGDLVPLSYIAGLLTGRPNSKATGPDGESLTAKEAFEKAGISTGFF}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           {\tt NITPCLPLRGTITASGDLVPLSYIAGLLTGRPNSKAVGPTGEVLNAEKAFAAAGVEGGFF}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GEKTKVAVTTKTLADPLNWGLAADQMKGSHLDEVKKMVEEYKRPVVNLGGETLT1GQVAA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       577; Conservative
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                        sequence.
                                                                                                          (first entry)
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99US-0161992.
99US-0161993.
99US-0162142.
                                                                                                                                                                 Protein;
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81.5%;
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                                                                                                                                                                   717
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28-SEP-1 29-SEP-1 04-OCT-1 05-OCT-1 06-OCT-1 07-OCT-1

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Matches
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  370 QATKSIEREINSVNDNPLIDVSRNKAIHGGNFQGTPIGVSMDNTRLAIAAIGKLMFAQFS
              364 SSTKMIEREINSVNDNPLIDVSRNKALHGGNFQGTPIGVSMDNTRLAIAAIGKLMFAQFS 423
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                                                                                                                                                                                  NITPCLPLEGTITASGDLVPLSYIAGLLTGPPNSKAVGPTGEVLNAEKAFAAAGVEGGFF
                                                                KHHPGQIEAAAIMEYILDGSDYVKAAQKVHEMDPLQKPKQDKYALKISPQWLGPQIEVIK
                                                                                                                                                                                                          QTELIRFLNAGIFGNTKETCHTLPQSATRAAMLVFVNTLLQGYSGIRFEILEAITSLLNH
                                                                                                                                                                                                                        QKELIKELNAGIFGNGIEISHILPHSATKAAMIVKINILLQGYSGIKFEILEAITKFINN 183
                                                                                                                                                                                                                                                           GEKTKVAVTTKTLADPLNWGLAADQMKGSHLDEVKKMVEEYRRPVVNLGGETLTIGQVAA 71
                                                    KHHPGQIEAAAIMEHILDGSSYMKLAQKVHEMDPLQKPKQDRYALRTSPQWLGPQIEVIR
                                                                                                      DLQPKEGLALVNGTAVGSGMASMYLFEANVQAVLAEVLSAIFAEVMSGKPEFTDHLTHKL
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81.5%; Pred. No. 5.2e-232;
81.5%; Mismatches 77;
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99US-0134219.

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99US-0134221.

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                                         Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control, promoter.
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                                            Arabidopsis thaliana protein fragment SEO ID NO: 67984.
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         mapping, gene expression control; promoter;
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                                                                                                                                                                   NVLALLSEVLSATFAEVMQGKPEFTDHLTHKLKHHPGGTEAAAIMEYTLJGSDYVKAAQK 331
                                                                                        LHEMDPLQKPKQDKYALRTSPQWLGPQIEVIRAATKMLEREINSVNDNPLIDVSRNKALH
                                                                                                                                                   NILAYLSEVMSAMFAEVMQGKPEFIDHLTHKLKHHPGGIEAAAIMEHILDGSSYVKEAQL 239
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                              GGNEQGTPIGVAMENSELAIASIGKLMEAQESELVNDEYNNGLESNLSGGRNPSLDYGEK
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                                                                                                                                                                                                                                                                                          Eucalyptus grandis
                                                                                                                                                                                                                                                                                                                         Pinus radiata; Monterey pine.
                                                                                                                                                                                                                                                                                                                                         Plant; lignin;
                                                                                                                                                                                                                                                                                                                                                                         Eucalyptus grandis PAL protein sequence SEQ ID NO 428
                                                                                                                                                                                                                                                                                                                                                                                                                                           AAH16402;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB16402 standard; Protein; 424 AA
Novel polynucleotide encoding enzymes involved in lignin-biosynthetic
                                  WP1; 2000-317962/27.
                                                                                             (GENE-) GENESIS RES & DEV CORP LTD. (FLET-) FLETCHER CHALLENGE FORESTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 RTSPQWLGPQ1EVIKQATKSIEKEINSVNUNPLIUVSKNKAIHGGNEQGTPIGVSMDNTR 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NPYTNHYQSAFQHNQDYNSIGI:ISAKKTAFAAVDII.KIMSSTYLVALIQQSIDI.RHLEENMK 528
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51.9%; Score 1892; DB 21; 83.7%; Pred. No. 3.9e~143;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 423;
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АВН78982 (I) АНН

АВВ78982 standard; Protein; 495 AA

ABB78982;

RESULT 15

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 biosynthetic pathway, and for producing a plant having altered lighth content, composition and structure. They can be used for designing probes and primers useful for detecting similar DNA and RNA sequences in any organism and for PGR amplification. The lighth content can be efficiently modified using the polynucleotides. AAA57908 to AAA68201 and AAB16341 to AAB16449 represent polynucleotide and protein sequences used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polynucleotides can be used for modulating lighin content, lighin composition and the structure of a plant, especially eucalyptus and pine species, and for modifying the activity of an enzyme involved in liquin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            coumerate COA ligase, cytochrome P450 LXXIA, diphenol oxidase, flavanol glucosyl transferase, flavenoid hydroxylase, and isoflavone reductase, which are involved in the lignin biosynthetic pathway. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             coniferol glucosyl transferase (CGT), coniferin beta-glucosidase (CBG), laccase, peroxidase, ferulate-5-hydroxylase (F5H), alpha-amylase, caffeic acid methyl transferase, caffeoyl CoA methyl transferase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes isolated polynocieotides and proteins encoding and representing the enzymes cinnamate 4-hydroxylase (C4H), commarate 3-hydroxylase (C3H), phomolase (PNL), G-methyl transferase (OMT), cinnamyl alcohol dehydrogenase (CAD), cinnamy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pathway useful for producing transgenic plants especially eucalyptus and pine species having altered lighin content, composition and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 18; Page 170-171, 213pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CCR), phenylaianine ammonia lyase (PAL), 4 coumarate:COA ligase (4CL),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         180
420 KIMFA 424
                                                                                         416 KIMPA 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          116 RTKGGGALQKELIRFLNAGIFGNGTETSHTLPHSATRAAMIVKINTLLQGYSGIRFEILE 175
                                                                                                                                                                             360 GPQIEVIRAATKMIEREINSVNDNPLIDVARNKALHGGNFQGTPIGVSMDNTRLAVASIG
                                                                                                                                                                                                                                                                      356 GPQTEVIRSSTRMIEREINSVNENPLIDVSRNKALHGGNFQGTPTGVSMDNTRIATAATG
                                                                                                                                                                                                                                                                                                                                                                300 TOHLTHKLKHHPGGIESAAIMEHILDGSAYVKAAKKLHEMDPLGKPKODRYALRTSPOWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             176 ATTKFLNNNTTPCLPLRGTTTASGDLVPLSYTAGLLTGRPNSKAVGPTGEVLNAEKAFAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 LITTAQVAAVAS---QEGVGVELSEAAKPRVKASSDWVMESMNKGTDSYGVTTGFGATSHR 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56 LTVSQVAGIAAANDSDTVKVELSEAARAGVKASSDWVMESMNKGIDSYGVITGEGATSHR 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MENGNHVNGVVNELCI-----KDPLNWGVAAEALTGSHLDEVKKMVAEERKPVVKLGGET 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 MESTTGTGNGLHSLCAAGSHHADPLNWGAAAAATGSHLDEVKPMVEEYPRPAVPLGGES 52
                                                                                                                                                                                                                                                                                                                                                                                                                           TDHLTHKLKHHPGQIEAAAIMEYILDGSDYVKAAQKVHEMDPLQKPKQDRYALRTSPQWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGIDTGFFELQPKEGLALVNGTAVGSGLASIVLFEANILAVLSEVLSAIFAEVMQGKPEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AITKELNHNITPCLPLPGTITASGDLVPLSYIAGLLTGPPNSKAVGPDGKSLLAVEAFRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RTKQGGALQKEL1RFLNAG1FGNGTESCHTLPQSSTRAAMLVRVNTLLQGYSG1RFE11.E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGVEGGFFELQPKEGLALVNGTAVGSGMASMVLFDANVLALLSEVLSALFAEVMQGKPEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       351;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49.4%; Score 1799; DB 21; Length 424; 82.6%; Pred. No. 1.1e-135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37; Mismatches
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           encoding caffeoyl-CoA 3-0-methyltransferase (CCOAMT), cinnamyl alcohol dehydrogenase (CAD), caffeic acid 0-methyltransferase (OMT), cinnamate-4-hydroxylase (C4H), cinnamoyl-CoA reductase (CCB), peroxidase (PELL), ferulate-5-hydroxylase (F5H), phenylalanine ammonia lyase (PAL) or 4-coumarate:CoA ligase (4CL) from perennial ryegrass (Lolium perennc) or fescue species. (1), its nucleotide sequence information and/or single nucleotide polymorphisms is useful as a molecular genetic marker. (1) can be used for modifying lighin biosynthesis and/or cellulose degradation in a plant to manipulate cell walls. (1) or its fragments are useful for isolating cDNAs and genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              encoding homologous proteins from the same or other plant species, as hybridisation probes to screen libraries from the desired plant. Short segments of (I) or its fragment are useful in amplification protocols
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 30; Fig 63; 436pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel nucleic acid encoding lignification and cellulase enzymes or their related enzymes useful for modifying lignin biosynthesis and cellulose degradation in plants to manipulate plant cell wall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-SEP 2000; 2000AU 0000419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cellulase; enzyme, lignin biosynthesis; cellulose degradation; ccommi; caffeoyl-CoA 3-0-methyltransferase; cinnamyl alcohol dehydrogenase; CAD; caffeic acid O-methyltransferase; OMT; cinnamate-4-hydrogenase; CAH; caffeic acid O-methyltransferase; OMT; cinnamate-4-hydrogenase; CAH; caffeic acid O-methyltransferase; CAH; caffeic acid O-methyltransferase; caffeic acid O-methy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lolium perenne; perennial ryegrass; plant; cell wall; lignification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lolium perenne LpPALa amino acid sequence SEQ ID No:141.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; ABN87223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lolium perenne.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes a nucleic acid (1) or its fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-SEF-2001; 2001WO-AU01221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lolium perenne (perennial ryegrass) amino acid sequence from the present
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                                                                   323 SÜYVKAAQKVHEMDPLQKPKQURYALKTSPQWLGPQ1EV1RSSTKMIEREINSVNDNPL1 382
                                                                                                                                                                                                                                                                                                                                                          263 MASMVI,FDANVLALLSEVI,SATFAFVMQGKPEFTDHLTHKI,KHHPGQIEAAAIMEYII,DG 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                   5 LASMVLFEANILSLLAEVLSAVFCEVMNGKPEFTDHLTHKLKHHPGQIEAAAIMEHILEG 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2002-444025/47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 344;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       495 AA;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sawbridge TI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48.8%; Score 1779; DB 23; Length 495; 76.6%; Pred. No. 5.7e-134;
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Sequence 13, Application US/09624693A Patent No. 6355468 GENERAL INFORMATION:
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APPLICANT: Havukkala, 11ka
TITLE OF INVENTION: Materials and Methods for the
TITLE OF INVENTION: Modification of Plant Lignin Content
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 25 SOFTWARE: PatentIn Ver. 2.0
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APPLICANT: Kootstra, Anna
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675 EELGVQARRGDVFVGVQQETIGSNVSRIYEAIKDGRINHVLVKML 719
                                                              661 EELG----RG-FLTGEKVTSPGEEFDRVFTAMCKGQIIDPLLECL 700
                                                                                                                            618 SANVTLTAVNAWKVASAEKAIS--LTREVRN-RFWQTPSSQAPAHAYLSPRTRVLYSFVR
                                                                                                                                                                                          602 TEKNTNTSI-FQKIATFEEELKVLLPKEVEGVRIAYENDTLSIPNRIKACRSYPLYRFVR 660
                                                                                                                                                                                                                                                                                                                    549 G-ELHPSKFCEKULLIRVVUKEY-----VFAYIUUVCSGFYPLMQKLKQVLVUHALNNGE 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           454 NRGLPSCLA-AEDPSLNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVNSLAL 512
                                                                                                                                                                                                                                                         573 ALALEVKKALNKRLEQTTTYDLEPRWHDAFSY----ATGT-------VVELLSSSP 617
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              216 SASGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEA--VVI.GPKEGLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NNGLPSNLSGGRNPSLDYGFKGGEIAMASYCSELQFLANPVINHVQSAEQHNQDVNSLGL 490
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; Sequence 19, Applications; Patent No. 6355468 US-09-624-693A-19

Sequence 19, Application US/09624693A

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Best Local :
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APPLICANT: Koolstra, Anna
TITLE OF INVENTION: Phenylalanine Ammonia Lyase Polypeptide and
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ORGANISM: Rhodotorula toruloides
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685 GKQEVT1-GSNVSKIYEAIKSGRINNVILKML 715
                                                                                                                                                                                                                                                                                                                                          542 FEFKK-----
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                                                                                                         625 WKVAAAESATSLTRQVRETFWSAASTSSPALSYLSPRTQTLYAFVREELGVKARRGDVFL 684
                                                                                                                                                              633 -RIAYENDTI.SIPNRIK-----ACRSYP------I.YRFVREELG----RG--FI. 668
                                                                                                                                                                                                                  566 GSNLRDELVE-KVNKTLAKRLEQTNSYDLVPRWHDAFSFAAGTVVEVLSSTSLSLAAVNA 624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    363 YPLRTSPQWIJPLVSNLIHAHAVLTTEAGQSTTDNPLIDVENKTSHHGGNEQAAAVANTM 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            245 YAREAMALFNIEF - VVLGPKEGIGIVNGTAVSASMATIALHDAHMISLISQSITAMTVE 302
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Local Similarity 35.9%; Pred. No. 4.9e-81;
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                                                                                                                                                                                                                                                                       MQKLRQVLVDHALANGETEKNTNTSIFQKIATFEEELKVLLPKEVEGV------632
                                                                                                                                                                                                                                                                                                                                                                                         ENMKSTVKNTVSQVAKKVLTMGVNGELHPSRFCEKDLLRVVDREYVFAYIDDVCSGTYPL 584
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                                                 TGEKVTSPGEEFDRVFTAMCKGQIIDPLLECL 700
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US-09-627-216A-8
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SOFTWARE: Microsoft Office 97
SEC ID NO 8
LENGTH: 716
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 270;
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566 GSNEKDELVE-KVNKTLAKRLEÖTNSYDLVPKWHDAFSFAAGTVVEVLSSTSLSLAAVNA 624
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                                                         585 MQKLRQVLVDHALNNGETEKNTNTSIFQKIATFEEELKVLLPKEVEGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            346 YALRTSPQWLGPQI-EVIRSSTKMIEREINSVNDNPLIDVSENKALHGGNEGGTPIGVSM 404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      303 AMVGHAGSFHPFLHDVTPPHPTQIEVAGNIRKLLEGSPFAVHHEFEVKVKDDEGILEQDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VMQGKP-EFTDHLTHKLKHHPGQIEAAAIMEYILDGSDY-VKAAQKVHEMDPLQKPKQDR 345
                                                                                                                                                                          ENMKSTYKNTYSQVAKKYLTMGYNGELHPSRFCEKDLLRYVDREYYFAY I DDYCSGTYPL 584
                                                                                                                                                                                                                                    GHLANPVTTHVQPAEMANQAVNSLALISARRTTESNDVLSLLLATHLYCVLQAIDLRAIE
                                                                                                                                                                                                                                                                                        QFLANPVTNHVQSAEQHNQDVNSLGLISARKTAEAVDILKIMSSTYLVALCQSIDLRHLE 524
                                                                                                                                                                                                                                                                                                                                                                                                         DNTFLATAATGKLMFAQFSELVNDFYNNGLESNLSGGRNESLDYGFKGGETAMASYCSEL
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                                                                                                                   ----QFGPA-----IVSLIDQHF------GSAMT 565
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 27.2%; Score 991.5; DB 4; Length 716; Best Local Similarity 35.9%; Pred. No. 9.2e-81; Matches 270; Conservative 122; Mismatches 251; Indels 109; Gaps
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SEQ ID NO 10
LENGTH: 716
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APPLICANT: Gatenby, Anthony
TITLE OF INVENTION: Bioproduction of para-Hydroxycinnamic Acid
FILE REFERENCE: BC1009 US NA
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ORGANISM: Artificial Sequence
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465 QFLANPYTNHVQSAEQHNQDVNSLGLISARKTAEAVDILKLMSSTYLVALCQSIDLRHLE 524
                                                       423 EKTRLGLAQIGKLNFTQLTEMLNAGMNRGLPSCLA-AEDPSLSYHCKGLDIAAAAYTSEL 481
                                                                                                                                                                                                                                                                                                                288 VMQGKP-EFTDHLTHKLKHHPGQIEAAAIMEYILDGSDY-VKAAQKVHEMDPLQKPKQDR 345
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                                                                                                            405 DNTRLAIAAIGKLMFAQFSELVNDFYNNGLPSNLSGGRNPSLDYGFKGGEIAMASYCSEL 464
                                                                                                                                                                    363 YPLRTSPQWLGPLYSDLIHAHAVLTIEAGQSTTDNPLIDVENKTSHHGGNFQAAAVANTM 422
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                                                                                                                                                                                                                                                                                                                                                                                               YAREAMALFNLEP--VVLGPKEGLGLVNGTAVSASMATLALHDAHMLSLLSQSLTAMTVE 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGALQKELIRFLNAGI------FGNGTETSHTLPHSATRAAMIVRINTLLQGYSGIR 170
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06 26	4 4	Qy Db	
347 366	290 QGKP-EFTDHLTHKLKHHÞGQIEAAAIMEYILDGSDY-VKAAQKVHEMDÞLQKÞKQDRYA 34 	Qy Db	
289 306	230 EKAFAAAGVEGGFFELQPKEGLALVNGTAVGSGMASMVLFDANVLALLSEVLSATFAEVM 21 ::     : :      : :      : :      : :        : :        : :        : :        : :        : :        : :        : :        : :        : :      : :          : :    : :        : :    : :      : :    : :    : :  : :    : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :	Qy Db	
229 248	170 RFEILEAITKFLNNNITPCLPLRGTITASGDLVPLSYIAGLI/TGRPNSKAVGPTGEVI.NA 2:   :  :    :    :   :	QY Db	
169 189	119 QGGALQKELIRFLNAGIFGNGTETSHTLPHSATRAAMIVRINTLLQGYSGI 16	QQ dd	
118 131	59 SQVAGIAAANDSDTVKVELSEAARĀGVKASSDWVMESMNKGTDSYGVTTGFGATSHRRTK 1	Qy Db	
ui čo	1 MENGNHVNGVVNELCI-KDPLNWGVAAEALIGSHLDEVKKMVAEF-RKPVVKLGGETLTV 5 :	Qy dd	
s 12	Query Match 26.7%; Score 971.5; DB 4; Length 713; Best Local Similarity 36.7%; Pred. No. 5.9e-79; Matches 267; Conservative 125; Mismatches 277; Indels 59; Gaps		
g and	SULT 7 -09-624-693A-17 -09-624-693A-17 -09-624-693A-17 -09-624-693A-17 -09-624-693A-17 -09-624-693A-17 -09-624-693A-17 -09-624-693A-17	US RE	
	685 GKQEVTI-GSNVSKIYEAIKSGRINNVLLKML 715	Db	
	669 TGEKVTSPGE	Qy	
84	625 WKVAAAESAISITRQVRETEWSAASTSSPALSYLSPRTQILYAFVREELGVKARRGDVFL 6	, Db	
O	633 -RIAYENDTLSIPNRIKACRSYPLYRFYREELGRGFL 6	Ç Ç	
32	585 MOKLROVLVDHALNNGETEKNTNTSIFOKIATFEEELKVLLPKEVEGV	Dh Qy	
65	542 FEFKK	Db	
84	525 ENMKSTVKNTVSQVAKKVLTMGVNGELHPSRFCEKDLLRVVDREYVFAYIDDVCSG	Оу	
41	482 GHLANPYTTHYQPAEMANQAVNSLALISARRTTESNDYLSLLLATHLYCYLQAIDLRATE 5	Db	

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Yoshida, Roberta
APPLICANT: Koolstra, Anna
TITLE OF INVENTION: Phenylalanine Ammonia Lyase Polypeptide and
TITLE OF INVENTION: Polypucleotide Sequences and Methods of Obt
TITLE OF INVENTION: Using Same
TITLE OF INVENTION: Using Same
TITLE REFERENCE: 29479/500NSC
CURRENT APPLICATION NUMBER: US/09/624,693A
CURRENT FILING DATE: 2000-07-24
NUMBER OF SEQ 1D NOS: 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: (12, 16, 17, 20, 24, 25, 28, 36, 38, 42, 47, 48, 56, 57, 62, 66, OTHER INFORMATION: "Xaa" means any amino acid: "Xaa" means no consensus at OTHER INFORMATION: position
OTHER INFORMATION: Description of Artificial Sequence: Consensus of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION. SEQ ID NOS: 13, 17, and 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        641 LSTPNRTK--ACRSYPLYREVREELG----RG--FLTGEKVTSPGEEFDRVFTAMCKGQ1 692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 593
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223 SPLSYIMMALTHHEDSKVIIVXHEGXEKIMXAFEAIALFGLEF VVLGPKEGILGLVNGTA
                                                                                                         165 NS--LPLEVVPGAMTIRVNSLTPGHSAVRLVVLEALTNFLNHGITPIVPLRGTISASGDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   467 LANPYTNHVQSAEQHNQDVNSLGLISARKTAEAVDILKLMSSTYLVALCQSIDLRHLEEN 526
                                                   202 VPLSYTAGILITGRPNSKA-VGPTG--EVLNAEKAFAAAGVEGGFFELQPKEGLALVNGTA 258
                                                                                                                                                               142 TSHTLEHSATRAAMIVRINTLLQGYSGIRFEILEAITKFLNNNITECLELRGTITASGDL 201
                                                                                                                                                                                                                            107 FLRXQLXNSV--YGVTTGFGGSADTRTEDATSLQKALLEHQLCGVLFTSXDSFXLGRGLE 164
                                                                                                                                                                                                                                                                               91 WVMESMNKGTDSYGVTTGFGATSHFRTKQGGALQKELIRFLNAGI-----FGNGTE 141
                                                                                                                                                                                                                                                                                                                                        49 TQLDIVEXXLADPXTDDXXELDGYSLTLGDVVG--AAPKGRXVRVXDSDEIRXKIDKSVE 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26.5%; Score 967; DP 4; Length 726; 36.9%; Pred No. 1 5e-78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches 262;
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187
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SEQ ID NO 327
LENGTH: 226
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                         Matches 182;
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PRIOR FILING DATE: 1997-11 21

PRIOR FILING DATE: 1996-09-11

PRIOR APPLICATE: 1996-09-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER.
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                       564 VVDREYVFAYILDDVISSIYPLMQKLRQVLVDHALNNGETEKNINISIFQKIATFEEELKV 523
                                                                                                                                                                                                                                               444 PSLDYGFKGGEIAMASYCSELQFLANPVTNHVQSAEQHNQDVNSLGLISAEKTAEAVDIL 503
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                                                                                                                                   504 KLMSSTYLVALCQSIDLRHLEENMKSTVKNTVSQVAKKVLTMGVNGELHFSRFGEKDLLR 563
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                                                                                 61 KLMSSTFLVALCQAIDLRHLEENLKSVVKNTVNQVAKKVLYVGSNGELHPSRFSEKDLIK 120
                                                                                                                                                                                                                                                                                                                                   Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YILDGSDY-VKAAQKVHEMDELQKEKQDRYALRTSPQWLGPQI-EVIRSSTKMIEREINS 375
                                                                                                                                                                                          PSIDYGEKGAEIAMASYCSELÜFLANPVINHVQSAEQHNQDVNSLGLISSRKTAEAIDVL 60
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80 5%; Pred. No. 6.9e-77;
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APPLICANT: Voshida, Roberta
APPLICANT: Kootstra, Anna
TITLE OF INVENTION. Phenylalanine Ammonia Lyase Polypeptide and
TITLE OF INVENTION: Polypucleotide Sequences and Methods of Obtaining and
TITLE OF INVENTION: Using Same
FILE REFERENCE: 29479/500NSC
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582 -----YPLMQKLRQVLVDHALNNGETEKNTNTSIFQKIATFEEELKVLLPKEVEGVRI 634
                                                          554 REFLPG-----LD111REELRSSPGSFLSSEQMEKLQQNLTSAFEDHLDKTTT 601
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                                                                                                                                                                             497 ---ATPGPTHIQSAEMHNQAVNSLALISARATITSLEVLTSLIASYLYILCQALDLRALQ 553
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      264 VLALHNIEP--FPLESKEPLGILNGTAFSASVAALALNEAIHLVLLAQVCTAMGTEALIG 321
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                                                                                                                                                                                                                                                                                                  EKTRLALHHVGKLLFSQSTELVNPAMNRGLPPSVA-ATDPSLNYHAKGLDIATAAYVAE- 496
                                                                                                                                                                                                                                                                                                                                                                                                                 PLRTSPQFLGPQIEDIISAFQTVTQECNYLPATDNPLIDGETGESHHGGNFQAMAVTNAM 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -KPEFTDHLTHKLKHHPGQIFAAAIMEYILDGSDYVKAAQ-KVHEM---DPLQKPKQDRY 346
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                                                                                                                  ENMKSTVKNTVSQVAKKVLTMGVNGELHPS--RFCEKDLLRVVDREYVFAYIDDVCSGT- 581
                                                                                                                                                                                                                                       QFLANPVINHVQSAEQHNQDVNSLGLISAKKTAEAVDILKLMSSTYLVALCQSIDLRHLE 524
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; Patent No. 6410718
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LENGTH: 164
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                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/615,192A CURRENT FILING DATE: 2000-07-12
                                                                                                                                                                                             APPLICANT: Bloksberg, Leonard N.
APPLICANT: Havukkala, Ilkaa
TITLE OF INVENTION: Materials and Methods for the
TITLE OF INVENTION: Modification of Plant Lignin Content
FILE REFERENCE: 11000.1003c4U
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                                           PRIOR APPLICATION NUMBER: US
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: US
PRIOR FILING DATE: 1996-09-11
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APPLICANT:
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NUMBER OF SEQ ID NOS.
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PRIOR FILING DATE:
                         PRIOR APPLICATION NUMBER:
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Havukkala, Ilkka
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  1998-10-09
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73.6%; Pred. No. 3e-51;
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                         us 09/169,789
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SOFTWARE: FastSEQ for Wind
SEQ ID NO 329
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                                                                                                                                                                                                  Sequence 331, Application MS/09615192A Patent No. 6410718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                               GENERAL INFORMATION:
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APPLICANT: Havukkala, Ilkka
TITLE OF INVENTION: Materials and Methods for the
TITLE OF INVENTION: Modification of Plant Lignin Content
FILE REFERENCE: 11000.1003c4U
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                FILE REFERENCE: 11000 1003c4U
CURRENT APPLICATION NUMBER: US/09/615,192A
CURRENT FILING DATE: 2000-07-12
                                                             TITLE OF INVENTION: Materials and Methods for the TITLE OF INVENTION: Modification of Plant Liquin Content FILE REFERENCE: 11000 1003c4U
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SOFTWARE. FastSEQ for Windows Version 3.0
PRIOR APPLICATION NUMBER:
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                               242 FEELÖPKECLALVNGTAVGSGMASMVLFDANVLALLS 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    182 NNNITPCLPLRGTITASGDLVPLSYIAGLLTGRPNSKAVGPTGEVLNAEKAFAAAGVEGG 241
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3EP: HS 08/975,316
US 08/975,316
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LENGTH: 132
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CURRENT FILING DATE: 1999-03-16
NUMBER OF SEQ ID NOS: 54
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TITUE OF INVENTION RECOMBINANT HAEMSPHILUS INFLUENZAE ALHESIN PROJEINS
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259 VGSGMASMVLFDANVLALLSEVLSATFAEVMQGKPEFTDHLTHKLKHHPGQTEAAATMEY 318
                                                                                                    572 GLLNLNEKNANKOPLVTDSTAATVGDLRKLGWVVSTKNGTKEESNOVKQADEVL-----F 626
                                                                                                                                                                                                                                                         514 NGGTTGTNT1--SVTKDGIKAGNKAITNVASGLRAYDDANFDVLNNSATDLNRHVEDAYK 571
                                                                                                                                                                                                                                                                                                                                                                                                                                                            396 GGKVAFTAKEDDKKKLVNAGDLVTALGNLSWKAKAFADTDTDGALEGISKDQEVKAGETV 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   347 ESGDGTTASVT----KDINGNGITVKYDAKVGDGLKFDSDKKIVAD-----TTALIVT 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58 VSQVAGIAA-----ANDSDTVKVELSEAARAGVKASSDWVMESMNKGTD-SYGVTT 107
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Local Similarity 20.7%; Pred. No. 0.34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 IKDPLNWGVAAEALTGSHLDEVKKMVAEFEKPVVKLGGETLTVSQVAGIAAANDSDTVKV 75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 ENGNHVNGVVNELCIKDFLNWGVA----AEALTGSHLDEVKKMVAEFRKPVVKLGGETLT 57
                                                TGAGAATVISKSENGKHITITVSVAETKALSGLEKLGDTIKLKVDNQNIDNVLTVGNNGTA 686
                                                                                                                                                                                                                                                                                                          GNGTETSHTLPHSATRAAM-----IVRINTLLQGYSGIRFEILEAITKFLNNNITPCL: 189
                                                                                                                                                                                                                                                                                                                                                             TEKAGKNIKVKQDGANFTYSIQDALTGITSITLGGTTNGGNDAKTVINKDGLTITPAG-- 513
                                                                                                                                                                                                                                                                                                                                                                                                              -----PLRGTITAS--GDLVPLSYIAGLLTG-RPNSKAVGPTGEVLNAEKAF 233
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rch con time	538 923	485 867	425 836	366 789	319 731	687
Search completed: March 29, 2003, 02:14:08 Job time : 43 secs	538 VAKKVLTMGVNGELHPSRFCEKDL 561	485 VNSLGLISARKTĀEAVDILKLMSSTYLVALCQSIDLRHLEENMKSTVKNTVSQ 537	425 LVNDFYNNGLPSNI.SGGRNPSLDYGFKGGEIAMASYCSEI.OFLANPYTNHVOSAFOHNQD 484 ::    :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :  :	366 TKMIEREINSVNDNPLIDVSRNKALHGGNFQGTPIGVSMDNTRLAIAAIGK-LMFAQFSE 424 	319 ILDGSDYVKAAQKVHEMDFLQKFKQDKYALKTSPQWLGPQIEVIRSS 365 	687 VTKGGFETVKTGATUADKGKVTVKDATANDADKKVATVKDVATA 730

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/cqn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
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/cgn2_6/ptodata/1/pubpaa/PcT_NEW_PUB.pep:*
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229.410 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

Result	Score	Query Match	Query Match Length DB	#0#	ID	Description
1	3644	100 0	711	٥	IIS-09-964-992A-1	i
ы	3290.5	اد (راد	713	د	IIS-09-964-992A-2	
w	3208	88.0	666	Ý	US-Ü9-964-992A-5	
4	2992	82.1	717	10	US · 09 · 854 · 122 · 49	
5	2728.5	74.9	7:00	-	US · U9 · B54 · 122 · 50	
6	1337	36.7	304	10	US-09-854-122-47	
7	1337	9 9k	303	:1	TIS-09-854-122 48	
8	1025	28.1	720	10	US-09-939-408A-13	
9	994.5	27.3	716	10	US-09-765-873A-8	
10	994.5	27.3	716	10	US-09-939-408A-19	
11	991 5	27 2	716	=	US-09-765-873A-10	
12	991.5	27 2	716	10	¤S+29+765+873 <b>A</b> +34	
13	990.5	27 2	716	ņ	US-09-765-873A-35	
14	990 5	27 2	716	10	US-09-765 873A-37	
15	988	27.1	686	10	US-09-765-873A-32	
16	986.5	27.1	716	<u>-</u>	US-09-765-873A-38	
17	984.5	27.0	716	10	US-09-765-873A-36	
18	5 086	26.9	716	10	118 U8-392-831-33	
19	971.5	26.7	713	10	US-09-939-408A-17	

,	44	43	42	41																					• :
455.5	458 5	461	461	467.5	468.5	469.5	473	476	476	479	489	489	501	502	202	508	513	517	518	521 5	527	529	844.5	917	7.74
12.5	12 6	12.7		12.8				13.1	13.1	13.1	13.4	13.4	13.7	13.8	139	13.9			14.2				:3 :2		3
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, .	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	-			Sequence	Sequence		Sequence	Sequence	Sequence	Sequence	Sequence	Sequence				Sequence	Sequence	autof.box
38, Appl	45, Appl	48, Appl	47, Appl	37, Appl	62, Appl	36, Appl	46, Appl	41, Appl	65, App)	52, Appl	12692, A	5671, Ap	53, <b>A</b> ppl		40, Appl	49, Appl	34, Appl		51, Appl	13990, A	50, Appl	12085, A	15, Appl	30, <b>∆</b> pp1	1ddv '17

## ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION. lettuce phenylalamine ammonia lyase (PAL) l; OTHER INFORMATION: (LsPAL1) US-09-964-992A-1
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                                                                                                                                                                                         Дb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 1, Application US/09964992A
; Patent No. US20020173633A1
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                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 3644; DB 9; Length 711; Best Inval Similarity 100.0%, Fred. N. 5.6-272; Matches 711; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Saltveit, Mikal E.
APPLICANT: Campos, Reinaldo
APPLICANT: No. USZÓÚZOT73633Alogaki, Hiroyuki
APPLICANT: Suslow, Trevor
APPLICANT: The Regents of the University of California
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Gene in Wounded Lettuce Tissue
FILE REFERENCE: 0.23070-12450003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/964,992A CURRENT FILING DATE: 2002-07-09 FRICK APPLICATION NUMBER: US 60/235,956 PRICK FILING DATE: 2000-09-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
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                            121 GALQKELIFFINAGIFGNGTETSHTLPHSATFAAMIVFINTLLQGYSGIRFEILEAITKF 180
                                                                          1 MENGNHVNGVVNELCIKDPLNWGVAAEALIGSHLDEVKKMVAEFFKPVVKLGGETLTVSQ 60
                                                                                                                                                                                                                   1 MENGNHYNGYVNELCIKDPLNWGYAAFALTGSHLDEYKKMYAEFRKPYVKLGGETLTVSQ 60
Indels 0;
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US-09-964-992A-2
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                                                                             Matches 645; Conservative
                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 2
LENGTH: 713
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Suslow, Trevor
APPLICANT: The Regents of the University of California
TITLE OF INVENTION. Characterization of Phenylaianine Ammonia-Lyase (PAL)
TITLE OF INVENTION: Gene in Wounded Lettuce Tissue
FILE REFERENCE: 023070-12450003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Saltveit, Mikal E
APPLICANT: Campos, Reinaldo
APPLICANT: No. US20020173633Alogaki, Hiroyuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/964,992A CURRENT FILING DATE: 2002-07-09
                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2000-09-26 NUMBER OF SEQ ID NOS: 13
                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/235,956
                                                                                                                                                                                                           OTHER INFORMATION: lettuce phenylalanine ammonia-lyase (PAL) OTHER INFORMATION: (LSPAL2)
                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                      ORGANISM: Lactuca sativa
                                                                                                                                                                                                                                                                                                                          TYPE: PRT
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                                                                                                         Local Similarity
                         1 MENGNHVNGVVNELCIK-DPLNWGVAAEALTGSHLDEVKKMVAEFRKPVVKLGGETLTVS 59
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                                                                             29; Mismatches
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US-09-964-992A-5
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                                                                                                                                             SEQ ID NO 5
LENGTH: 666
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                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Suslow, Trevor
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Characterization of Phenylalanine Ammonia-Lyase (PAL)
TITLE OF INVENTION: Gene in Wounded Lettuce Tissue
FILE REFERENCE: 023070-124500US
                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/964,992A CURRENT FILING DATE: 2002-07-09 PRIOR APPLICATION NUMBER: US 60/235,956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Saltveit, Mikal E.
                                                                                                                                                                                                         SOFTWARE:
                                                                                                                                                                                                                                     PRIOR FILING DATE: 2000-09-26 NUMBER OF SEQ ID NOS: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                         OTHER INFORMATION: sunflower phenylalanine ammonia-lyase (PAL)
                                                           FEATURE:
                                                                              ORGANISM: Helianthus annuus
                                                                                                                       TYPE. PRT
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No. US20020173633Alogaki, Hiroyuki
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                       SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 49
LENGTH: 717
TYPE: PRT
                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                           Sequence 49, Application US/09854122 Patent No. US20020016980A1
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                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/854,122 CURRENT FILING DATE: 2001-09-10
                                                                                                                                                                                                                                                APPLICANT: ALBERTE, RANDALL S.
APPLICANT: SMITH, ROBERT
TITLE OF INVENTION: TRANSGENTO PLANTS INCORPORATING TRAIT OF ZOSTERA MARINA
                                                                                                                                   PRIOR APPLICATION NUMBER: 50/202,529 PRIOR FILING DATE 2000-05 10
                                                                                                                                                                                                                             FILE REFERENCE: PHA-007.01
                                                                                                                  NUMBER OF SEC ID NOS: 51
ORGANISM: Arabidopsis thaliana
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                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: ALBERTE, RANDALL S.
APPLICANT: SMITH, ROBERT
APPLICANT: SMITH, ROBERT
TITLE OF INVENTION: TRANSGENIC PLANTS INCORPORATING TRAIT OF ZOSTERA MAKINA
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 50
LENGTH: 700
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 50, Application US/09854122 Patent No. US20020016980A1
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                                                                                                             FILE REFERENCE: PHA-007.01
CURRENT APPLICATION NUMBER: US/09/854,122
CURRENT FILIN: CATE 2:01-09-10
PFICE APPLICATION NUMBER: 50/202.529
PRICE FILING DATE 2:000-05-10
                                                                                           NUMBER OF SEQ ID NOS: 51
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US-09-854-122-47; Sequence 47, Application US/09854122; Patent No. US20020016980A1
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                         SEQ ID NO 47
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                                                                                                    TITLE OF INVENTION: TRANSGENIC PLANTS INCORPORATING TRAIT OF ZOSTEKA MARINA FILE REFERENCE: PHA-007.01

CURRENT APPLICATION NUMBER: US/09/854,122

CURRENT FILING DATE 2001-09-10

PRIOR APPLICATION NUMBER: 60/202,529

PRIOR APPLICATION NUMBER: 60/202,529

PRIOR FILING DATE: 2000-05-10
                                                    SOFTWARE: PatentIn Ver. 2.1
                                                                        PRIOR FILING DATE: 2000-05-10
NUMBER OF SEQ ID NOS: 51
                                                                                                                                                                                                                                                                   APPLICANT: ALBERTE, RANDALL S. APPLICANT: SMITH, ROBERT
LENGTH: 304
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                                                                                                                                                                                                                                                                SMITH, ROBERT
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US-09-854-122-48
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US-09-854-122-48
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PRIOR FILING DATE: 2000-05-10
NUMBER OF SEV ID NUS: 51
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 48
LENGTH: 303
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                              579 SGTYPI.MQKLRQVLVDHALNNGETEKNTNTSIFQKIATFEEELKVLLPKEV 629
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253 SATYPLMQKLRSVLVDHALNNGDKEKDEAMSIFQKIAVFEEELIAVFPKEV 303
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SEQ ID NO 13
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APPLICANT: Kootstra, Anna
TITLE OF INVENTION: Phenylalanine Ammonia Lyase Polypeptide and
TITLE OF INVENTION: Polynucleotide Sequences and Methods of Obtaining and
TITLE OF INVENTION: Using Same
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LOCATION: (153)
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                       549 G-ELHESRECEKDILLKYVDKEY-----VFAYIDDYCSCIYPLMQKI.KQVI.VDHALNNGE 601
                                                                              513 ISARRTAEANDVLSLLLASHLYCTIQAVDLRAMELDEKKQEDPLLPTLLQQHLGTGLDVN 572
                                                                                                                                  491 ISARKTAEAVDILKLMSSTYLVALCQSIDLRHLEENMKSTVKNTVSQVAKKVLTMG--VN 548
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/147,719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 39/627,216 PRIOR FILING DATE: 2000-07-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/765,873A CURRENT FILING DATE: 2001-01-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION. BIGPRODUCTION OF PARA-HYDROXYCINNAMIC ACTO FILE REFERENCE: BC1009 US CIP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Rhodotorula glutinis
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482 GHLANPVTTHVQPAEMANQAVNSLALISAKKTTESNDVLSLILLATHLYCVLQALDI.RAIE 541
                                                         465 QFLANPVTNHVQSAEQHNQDVNSLGLISARKTAEAVDILKLMSSTYLVALCQSIDLRHLE 524
                                                                                                                                                                           405 DNTRLATAATGKLMFAQFSELVNDFYNNGLPSNLSGGRNPSLDYGFKGGETAMASYCSEL 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           185 LVVLEALTNFLNHGITPIVPLRGTISASGDLSPLSYIAAAISGHPDSKVHVVHEGKEKIL
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                                                                                                                                                                                                                                           363 YPLPTSPQWLGPLVSDLTHAHAVLTIEAGQSTTDNPLIDVENKTSHHGGNFQAAAVANTM 422
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                                                                                                                     EKTRLGLAQIGKLNFTQLTEMLNAGMNRGLPSCLA-AEDPSLSYHCKGLDIAAAAYTSEL 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YAREAMALENLEP - - VVI.GPKEGLGLVNCTAVSASMATLALHDAHMLSLLSQSLTAMTVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAEKAFAAAGVEGGFFELQPKEGLALVNGTAVGSGMASMVLFDANVLALLSEVLSALFAE 287
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                                                                                                                                                                                                                                                                                                                                                                                                                      VMQGKP-EFTDHLTHKLKHHPGQIEAAAIMEYILDGSDY-VKAAQKVHEMDPLQKPKQDR 345
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US-09-939-408A-19
Sequence 19, Application US/09939408A
; Patent No. US20020102712A1
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APPLICANT: Kootstra, Anna
TITLE OF INVENTION: Phenylalanine Ammonia Lyase Polypeptide and
TITLE OF INVENTION: Polynucleotide Sequences and Methods of Obtaining and
TITLE OF INVENTION: Using Same
FILE REFERENCE: 29479/500NSCA
CURRENT APPLICATION NUMBER: US/09/939,408A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US/09/624,693
PRIOR APPLICATION NUMBER: US/09/624
PRIOR APPLICATION NUMBER: US/09/07-24
PRIOR APPLICATION NUMBER: PCT/US01/23270
PRIOR FILING DATE: 2001-07-24
NUMBER OF SEC 10. NOC. 20
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SOFTWARE: PatentIn Ver. 2.0
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363 YPLRTSPQWLGPLVSDLIHAHAVLTIEAGQSTTDNPLIDVENKTSHHGGNFQAAAVANTM 422
                                                             346 YALRTSPOWLGPQI-EVIRSSTKMIEREINSVNDNPLIDVSRNKALHGGNFQGTPIGVSM 404
                                                                                                                              303 AMVGHAGSFHPELHDVTRPHPTQIEVAGNIRKLLEGSRFAVHHEEEVKVKDDEGILRQDR 362
                                                                                                                                                                                                                                                                                                                                                                                                                               171 FEILEAITKFLNNNITPCLPLRGTITASGDLVPLSYIAGLLTGRPNSKA-VGPTG--EVL 227
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                                                                                                                                                                                              288 VMQGKP-EFTDHLTHKLKHHPGQIEAAAIMEYILDGSDY-VKAAQKVHEMDPLQKPKQDR 345
                                                                                                                                                                                                                                                               245 YAREAMALENLEP--VVLGPKEGLGLVNGTAVSASMATLALHDAHMLSLLSQSLTAMTVE 302
                                                                                                                                                                                                                                                                                                                                228 NAEKAFAAAGVEGGFFELQPKEGLALVNGTAVGSGMASMVL/FDANVLALLSEVLSAIFAE 287
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Local Similarity 35.9%; Pred No 3.2e-58;
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VKAAQKVHEMDPLQKPKQDR 345	8 VMQGKP-EFTDHLTHKLKHHPGQIEAAAIMEYILDG	Qy 281	
DAHMLSLLSQSLTAMTVE 302	5 YAREAMALENLEPVVLGPKEGLGLVNG	Db 24!	
DANVIALI,SEVLSAIFAE 287	NAER	Qу 228	
GRPNSKA-VGPTGEVL 227    :       ::  GHPDSKVHVVHEGKEKIL 244	1 FEILEAITKFLNNNITPCLPLRGTITASCDLVPLSYIAGLLTGRPNSKA-VGPTG	Qy 171 Db 185	
FGNGTETSHTLPHSATRAAMIVRINTLLQGYSGIR 170	GGALQKELIRFLNAGI	Qy 120 Db 127	
SYGVTTGFGATSHRRTKQ 119            : -YGVTTGFGGSADTRTED 126	0 QVAGIAAANDSDTVKVELSEAARAGVKASSDWVMESMNKGTDSYGVTTGFGATSHRRTKQ 	Qy 60 Db 71	
DEVKKMVAEFRKPVVKLGGETLTVS 59     :     :     :     :     :       :	8 NGVVNELCIKDPLNWGVAAEALTGSHLDEVKKMVAEERKPVVKLGGET	0y 1	
DB 10; Length 716; 668; 251; Indels 109; Gaps 2	y Match 27.2%; Score 991.5; Local Similarity 35.9%; Pred. No. 5.56 thes 270; Conservative 122; Mismatches	Query M Best Lo Matches	
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	R OF SEQ ID NOS: 38  ARE: Microsoft Office 97  NO 10	NUMBER OF SOFTWARE:	
	THE APPLICATION NUMBER: US 09/627,2  OR FILING DATE: 2000-07-27  OR APPLICATION NUMBER: US 60/147,7  OR FILING DATE: 1999-08-06	PRI	
	)9 US CIP NUMBER: US/09/76 2001-01-19	CUR	
DRUXYGINNAMIC ACID	OF INVENTION: BIOPRODUCTION OF	GENE APP	
	SULT 11 -09-765-873A-10 Sequence 10, Application US/09765873A	S E	
	5 GKQEVTI-GSNVSKIYEAIKSGRINNVLLKML	Db 68	
	9 TGEKVTSPGEEFDRVFTAMCKGQIIDPLLECL	Qy 66	
YLSPRTQILYAFVREELGVKARRGDVFL 684	S WKVAAAESAISLTRQVRETFWSAASTSSPALS	Db 62	
LYRFVREELGRGFL 668	3 -RIAYENDTLSIPNRIKACRSYP-	Qу 63	• -
. FAAGTVVEVLSSTSLSLAAVNA 624	z	56	
ELKVLLPKEVEGV 632	5 MQKLRQVLVDHALNNGETEKNTNTSIFQKIAT	Qу 58	
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                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                        Matches 270;
                                                                                                                                                                                                                                                       OTHER INFORMATION: x= Thr. Ala. Ser. Pro. Gly (-09-765-873A-34)
                                                                                                                                                                                   Best.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 1999-08-06 NUMBER OF SEQ ID NOS: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/147,719
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/765,873A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Microsoft Office 97
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                                                                                                                                                                                                                                                                                                                                                    LOCATION: (138)..(138)
OTHER INFORMATION: x- Leu, Met, Ile, Val, Cys
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60 QVAGIAAANDSDTVKVELSEAARAGVKASSDWVMESMNKGTDSYGVTTGFGATSHRRTKQ 119
                                                  14 NGVAS---AKQAVNGASTNI.AVAGSHLÆTTÖVTÖVDI VEKMLAAPIDSILELDGYSI.NI.G 70
                                                                                                                                                                              Local Similarity
                                                                                                 8 NGVVNELCIKDPLNWGVAAEALTGSHL-------DEVKKMVAEERKPVVKLGGETLITVS 59
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                                                                                                                                                                        27.2%, Score 991.5, DB 1 35.9%; Pred. No. 5.5e-68;
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                                                                                                                                                                                                   DB 10, Length 716,
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Sequence 35, Application US/09765873A
Patent No. US20010053847A1
GENERAL INFORMATION
APPLICARM
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                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 09/627,216 PRIOR FILING DATE 2000-07-27
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TITLE OF INVENTION: BIOPPOINTION OF PAPA-HYDROXYCINNAMIC
                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: BC1009 US CIP
                 COCATION: (198)..(198)
OTHER INFORMATION: X= Asp, Asn, Glu, Gln
                                                                                                                                     ORGANISM: mutant from Rhodotorula
                                                                                                                                                                  TYPE. PRT
NAME/KEY: UNSURE
                                                                              NAME/KEY: UNSURE
                                                                                                              FEATURE:
                                                                                                                                                                                          LENGTH: 716
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RESULT 14
US-09-765-873A-37
; Sequence 37, Application US/09765873A
; Patent No. US20010053847A1
; Patent No. US20010053847A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Xiao-Song
; TITLE OF INVENTION: BIOPRODUCTION OF PARA-HYDROXYCINNAMIC ACID
; FILE REFERENCE: BC1009 US CIP
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CURRENT APPLICATION NUMBER: US/09/765,873A CURRENT FILING DATE: 2001-01-19 PRIOR APPLICATION NUMBER: US 09/627,216 PRIOR FILING DATE: 2000-07-27
                                                                                                                                                                                                                                                                                                                                                                                                                 685 GKQEVTI-GSNVSKIYEAIKSGRINNVLLKML 715
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -RIAYENDTLSIPNRIK-----ACRSYP------LYRFVREELG----RG--FL 668
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 270; Conservative 122; Mismatches 251; Indels 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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LOCATION: (540)...(540)
OTHER INFORMATION: X= Thr, Ala, Ser, Pro, Gly
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LOCATION. (202)...(202)
OTHER INFORMATION: X= Val, Met, Leu, Cys
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669 TGEKVTSPGEEFDRVFTAMCKGQIIDPLLECL 700
                                                     625 WKVAAAESAISLTRQVRETFWSAASTSSPALSYLSPRTQILYAFVREELGVKARRGUVFL 684
                                                                                                                                                                    566 GSNLRDELVE-KVNKTLAKRLEQTNSYDLVPRWHDAFSFAAGTVVEVLSSTSLSLAAVNA 624
                                                                                                                                                                                                                                                                                                                                                                                                     482 GHLANPVTTHVQPAEMANQAVNSLALISARRTTESNDVLSLLLATHLYCVLQAIDLRAXE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               363 YPLRTSPQWLGPLVSDLIHAHAVLTIEAGQSTTDNFLIDVENKTSHHGGNFQAAAVANTM 422
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                                                                                                                                                                                                                          585 MQKLRQYLVDHALNNGETEKNTNTSIFQKIATFEEELKYLLPKEVEGV~--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    288 VMQGKP-EFFEHLFHKLKHHPGQIEAAAIMEYILDGSDY-VKAAQKVHEMDPLQKPKQUR 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      228 NAEKAFAAAGVEGGFFELQPKEGLALVNGTAVGSGMASMVLFDANVLALLSEVLSAIFAE 287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YALRTSPQWLGPQI-EVIRSSTKMIEREINSVNDNPLIDVSRNKALHGGNFQGTPIGVSM 404
                                                                                                              -RIAYENDTI,SIPNRIK----ACRSYP------I,YRFVREELG----RG--FL 668
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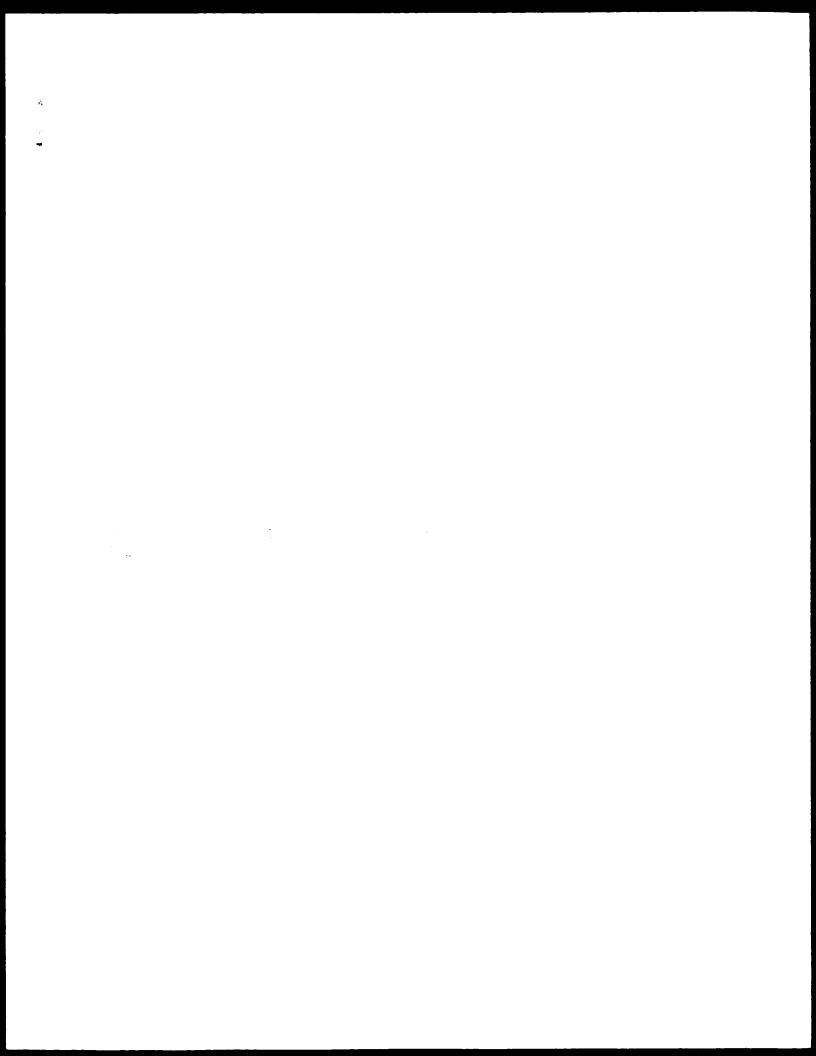
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: mutant from Rhodotorula glutinis US-09-765-873A-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-765-873A-32

: Sequence 32, Application US/09765873A

: Patent No. US20010053847A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Tang, Xiao-Song
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 265;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 2000-07-27
PRIOR APPLICATION NUMBER: US 60/147,719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT FILING DATE: 2001-01-19
PRICE APPLICATION NUMBER: US 09/627,216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/765,873A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: BIOPPOPULATION OF PARA-HYDROXYCINNAMIC ACID FILE REFERENCE: BC1009 US CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ 1D NOS: 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 686
555 LEQTNSYDLVPRWHDAFSFAAGTVVEVLSSTSLSLAAVNAWKVAAAESAISLTRQVRETF 614
                                                            605 NTNTSIFQKIATFEEELKVLLPKEVEGV----
                                                                                                                                                                                                                                   472 VNSLALISARRTTESNDVLSLLLATHLYCVLQAIDLRAIEFEFKK---
                                                                                                                                                                                                                                                                                       485 VNSLGLISARKTAEAVDILKLMSSTYLVALCQSIDLRHLEENMKSTVKNTVSQVAKKVLT 544
                                                                                                                                                                                                                                                                                                                                                 413 MI.NAGMNRGI.PSCI.A-AEDPSI.SYHCKGI.DIAAAAYTSEI.GHI.ANPYTTHVQPAEMANQA 471
                                                                                                                                                                                                                                                                                                                                                                                  425 LVNDFYNNGLPSNLSGGRNPSLLYGFKGGEIAMASYCSELQFLANPVTNHVQSAEQHNQD 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 353 HAVLTIEAGQSTTDNPLIDVENKTSHHGGNFQAAAVANTMEKTRLGLAQIGKLNFTQLTE 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        365 STKMIERHINSVNDNPLIDVSRNKALHGGNFQGTPIGVSMDNTRLAIAAIGKLMFAQFSE 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    293 PTQIEVAGNIRKLLEGSRFAVHHEEEVKVKDDEGILRQDRYPLRTSPQWLGPLVSDLIHA 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     307 PGÜLEAAAIMEYILDGSDY-VKAAQKVHEMDPLQKPKQDRYALKTSPQWLGPQI-EVIRS 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               233 KEGLGLVNGTAVSASMATLALHDAHMLSLLSQSLJTAMTVEAMVGHAGSFHPFLHDVTRPH 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      248 KEGLALVNGTAVGSGMASMVLFDANVLALLSEVLSAIFAEVMQGKP-EFTDHLTHKLKHH 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               175 LRGTISASGDLSPLSYIAAAISGHPDSKVHVVHEGKEKILYAREAMALFNLEP--VVLGP 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         191 LRGTTTASGDLVPLSYTAGLLTGRPNSKA-VGPTG--EVLNAEKAFAAAGVEGGFEELQP 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117 FDSFRLGRGLENS--LPLEVVRGAMTIRVNSLTRGHSAVRLVVLEALTNFLNHGITPIVP 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      136 -----FGNGTETSHTLPHSATRAAMIVRINTLLGGYSGIRFEILEAITKFLNNNITPCLP 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             / Match 27.1%; Score 988; DB 10; Length 686;
Local Similarity 36 2%; Pred No. 9.6e-68;
hes 265; Conservative 121; Mismatches 240; Indels 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59 EIRSKIDKSVEFLRSQLSMSV--YGVTTGFGGGADTRTEDAISLQKALLEHQLCGVLPSS 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80 AARAGVKASSDWVMESMNKGTDSYGVTTGFGATSHPRTKQGGALQKELIRFLNAGI---- 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28 ALTGSHL------DEVKKMVAEFKKPVVKLGGETLTVSQVAGTAAANDSDTVKVELSE 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AVAGSHLPTTQVTQVDIVEKMLAAPTDSTLELDGYSLNLGDV--VSAARKGRPVRVKDSD 58
                                                                                                                                                                       MGVNGELHPSRECEKDLLRVVDREYVEAYIDDVCSGTYPLMQKLRQVLVDHALNNGETEK 604
                                                                                                                   ----QFGPA-----IVSLIDQHF----
                                                                                                                      -----GSAMTGSNLRDELVE-KVNKTLAKR 554
                                                            ------- RIAYENDTLSIPNRIK--- 648
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Title:
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Maximum Match 100%
Listing first 45 summaries
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PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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3644
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GenCore version 5 1.4.p5_4578 Copyright (c) 1993 - 2003 Compagen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                    IIDPLLECEGGWNGEPEPIC 711
                                                                                                                                                                                                                                                           283224
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

29	28	27	26	125	24	23	: :	21	20	19	18	17	16	15	14	13	12	11	10	9	œ	7	6	ر ت	4	w	2	_		Result	•
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phenylalanine ammo	phenylalanine ammo	phenylalanine ammo	phenylalanine ammo				phenylalanine ammo				phenylalanine ammo	phenylalanine ammo		phonylalanine ammo		phenylalanine ammo										phenylalanine ammo	phenylalanine ammo	phenylalanine ammo	Description		

histidine ammonia-	2 E82228		<u>_</u>	14.8	540.5	45
phenylalanine ammo	2 501999	نیا	71	26.7	971.5	44
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phenylalanine ammo	2 A56628	· .	716	27 3	994 5	41
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probable phenylala	2 T05968	7	4 9	51.8	1887	38
phenylalanine ammo	2 101966	ci	47	13. IS	1948	17
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phenylalanine ammo	S28185	6	71	70.1	2555.5	0

## ALIGNMENTS

	Qy 361	Фу 301 Db 301	Фу 241 Db 241	Оу 181 Db 181	Qy 121 Db 121	©у 61 ръ 61	Фy	query M Best Lo Matches	r12749 r12749 phenylalani C; Species: C; Spate: IJ C; Accession R; Mazeyrat, submitted t A; Reference A; Reference A; Rosidues: A; Cross ref C; GenetLes: A; Gene: PAL C; Superfami C; Keywords: F; 197-199/C F; 198/Modif
		1. HKLKHHPGQIEAAAIMEYILGGSDYVKAAQKVHEMDFDQKFKQDKYALKISFQWLGPQIE 360	1 GFFELGPKEGLALVNGTAVGSGMASMVLFDANVLALLSEVLSATFAEVMOGKPEFTDHLT 300 	1 :NNNITPCLELEKCITASGULVELSYTAGLLIGEENSKAVGETGEVILNAENAFAAAGVEG 240 	1. GALGKELIRELNAGIFGNGTETSHTLFHSATRAAMIVKINTILLGIYSGIRFEILEAITKF. 180 	1 VAGTAAANISDIVKVELSEAAKAGVKASSIMVMESMIKGTISVGVTTGEGGATSHPRIKGG 120 	1 MENGNHVNGVVNELCIKUPLNWGVAAFALTGSHIDEVKKMVAEFRKIPVVKLGGEILTVSO 60 	uery Match 68.0%; Score 3.06; DB 2; Length 667; est Local Similarity 94.4%; Pred. No. 1.1e-197; atches 627, Conservative 13; Mismatches 24; Indels 0; Gaps 0	RESULT 1 T12749 phenylalanine ammonia·lyase (EC 4.3.1.5) · common sunflower C;Species: Helianthus annuus (common sunflower) C;Accession: T12749 R;Mazeyrat, F.A. submitted to the EMBL Data Library, February 1998 A;Reference number: Z17579 A;Accession: T12749 A;Accession: T12749 A;Accession: T12749 A;Mclecule type: mRNA A;Mclecule type: mRNA A;Mclecule type: mRNA A;Mclecule type: mRNA A;Residues: 1-667 <maz> A;Acne: PAL C;Genetics: ammonia-lyase C;Reywords: ammonia-lyase; carbon-nitrogen lyase C;Superfamily: histidine ammonia-lyase C;Superfamily: histidine ammonia-lyase F;197-199/Cross-link: 5-imidazolinone (Ala-Gly) #status predicted F;198/Modified site: dehydroalanine (Ser) #status predicted</maz>

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C;Keywords: ammonia-lyase; carbon-nitrogen lyase
F;202-204/Cross-link: 5-inidazolinone (Ala-Gly) #status pred
F;203/Modified site: dehydroalanine (Scr) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C:Species: Petroselinum crispum (parsley)
C:Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 21-May:1494
C:Accession: S04463
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A:Molecule type: DNA
A:Residues: 1 716 <LOT>
A:Cross-references: EMBL:X15473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R:Lois, R.; Dietrich, A.; Hahlbrock, K.; Schulz, W. EMBO J. 8, 1641-1648, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            phenylalanine ammonia-lyase (EC 4.3.1.5) - parsley
C; Species: Petroselinum crispum (parsley)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: A phenylalanine ammonia-lyase gene from parsley: structure, A;Reference number: S04463, MUID.89356635, PMID:2767049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: S04463
                                                                                                                                                                                                            233 FAAAGVEGGFFELQPKEGLALVNGTAVGSGMASMVLFDANVLALLSEVLSAIFAEVMQGK 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         481
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                                                                                                                                                                                                                                                                                                                     173 ILEAITKFLNNNITPCLPI.RGTITASGDLVPLSYIAGLLTGRPNSKAVGPTGEVLNAFKA 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      661 EELG 664
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                        353 QWLGPQIEVIRSSTKMIEREINSVNDNPLIDVSRNKALHGGNFQGTPIGVSMDNTRLAIA 412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 GETLTISQVAAI-SARDGSGVTVELSEAARAGVKASSDWVMDSMNKGTDSYGVTTGFGAT 119
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3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GETLTVSQVAGIAAANDSDTVKVELSEAARAGVKASSDWVMESMNKGTDSYGVTTGFGAT 112
                                                                                                                                                                                                                                                                                                                                                                                               SHRRTKQGGALQKELIRFLNAGIFGNGSD--NTLPHSATRAAMLVRINTLLQGYSGIRFE 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SHRRTKQGGALQKELIRFLNAGIFGNGTETSHTLPHSATRAAMIVRINTLLQGYSGIRFE 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ETEKNANTSIFQKIATFEDELKAILPKEVESVRVAFENGTMSIPNRIKACRSYPLYRFVR 660
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                                                                             PEFTDHLTHKLKHHPGQIEAAAIMEHILDGSAYVKAAQKLHEMDPLQKPKQDRYALRTSP
                                                                                                                               PETTDHLTHKLKHHPGQIEAAAIMEYILDGSDYVKAAQKVHEMDPLQKPKQDRYALRTSP 352
                                                                                                                                                                                      FKLAGVEGGFFELQPKEGLALVNGTAVGSGMASMYLFEANILAVLAEVMSAIFAEVMQGK
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                                                                                                                                                                                                                                                                                         ILEAITKFLNQNITPCLPLRGTTTASGDLVPLSY1AGLLTGRPNSKAVGPTGVILSPEEA
620;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87.4%; Score 3186.5;
86.2%; Pred. No. 2.3e
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Db Db Db

187 240

121 127

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Qγ
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C;Keywords: ammonia-lyase; carbon-nitrogen lyase
F;204-206/Cross-link: 5-imidazolinone (Ala-Gly) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     phenylalanine ammonia-lyase (EC 4.3.1.5) 3 - parsley
C;Species. Petroselinum crispum (parsley)
C;Date: 18-Oct-1995 #sequence_revision 12-Apr-1996 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Qy
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                                                                                                                                                                                                                                                                                                   F; 205/Modified site: dehydroalanine (Ser) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-58, 'E', 60-718 <APP2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                submitted to the EMBL Data Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-718 < APP1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Title: Structural and catalytic properties of the four phenylalanine ammonia-lyase A; Reference number: S48725; MUID:95010141; PMID:7925471 A; Accession: S48726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 В
                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: PAL3
                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross references. EMBL.X81159; NID:g535007, PIDN:CAA57057.1; PID.g535008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: S56035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Reference number: S56035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R; Appert,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references: EMBL: X81159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R; Appert, C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Accession: S48726; S56035
                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                 Query Match
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61 VAGIAAANDSDTVKVELSEAARAGVKASSDWVMESMNKGTDSYGVTTGFGATSHRRTKQG 120
                                                                                                                                                                                                                      Loca I
                                                                                                                                3 NGNHVNGVVNELCIK--DPLNWGVAAEALTGSHLDEVKKMVAEFRKPVVKLGGETLTVSQ 60
                                                                          NG-HANGNGLDLCMKKEDPLNWGVAAEALTGSHLDEVKRMVAEYRKPVVKLGGETLTISQ 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YPLYKFVRKELGTEYLTGEKVTSPGEEFEKVFIAMSKGEIIDPLLECLESWNGAPLPIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VDHALNNGETEKNTNTSIFQKIATFEEELKVLLPKEVEGVPIAYENDTLSIPNPIKACPS 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NTVSSVAKRVLTMGVNGELHPSRFCEKDLLRVVDREYIFAYIDDPCSATYPLMQKLRQTL 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NHVQSAEQHNQDVNSLGLISSRKTSEAVEILKLMSTTFLVGLCQAIDLRHLEENLKSTVK 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NHVQSAEQHNQDVNSLGLISARKTAEAVDILKLMSSTYLVALCQSIDLRHLEENMKSTVK 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QWLGPQIEVIRSSTKMIEREINSVNDNPLIDVSRNKAIHGGNFQGTPIGVSMDNTRLAIA 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VEHALKNGDNERNLSTSIFQKIATFEDELKALLPKEVESARAALESGNPAIPNRIEECRS 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NTVSQVAKKVLTMGVNGELHPSRFCEKDLLRVVDREYVFAYIDDVCSGTYPLMQKLRQVL 592
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                                                                                                                                                                                           621;
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                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                87.48;
87.28;
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                                                                                                                                                                                                                Pred. No. 2
                                                                                                                                                                                                                                              Score 3186.5; DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                August 1994
                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                      .3e-196;
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                                                                                                                                                                                        Indels
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phenylalanine ammonia-lyase (EC 4.3.1.5) 2 - parsley C.Spectes: Petroselinum crispum (parsley) C.Spectes: Petroselinum crispum (parsley) C.Spectes: Petroselinum crispum (parsley) C.Spectes: Petroselinum crispum (parsley) C.Spectes: 28 Oct: 1995 #scquence.revision 10 Nov:1995 #tcxt_change 16-Jui-1999 C.Accession: \$48725 R.Appert, C.: Lodemann. E. Hallfrowk, K Schmid. T. Amrh-in, N Eur. J Blochem 255, 49140, 1994 A.Tille: Structural and catalytic properties of the four phenylalanine ammonia-lyase isd A.Accession: \$48725 A.Status: nucleic acid sequence not shown A.Molecule Lype: makh A.Pesidues: 1.716: App. A.Scress reletences: EMBLIXB115R: NID-9634892: PIDN:CAA57056 1: PID:9534893 A.Sesidues: 1.716: App. A.Cross reletences: EMBLIXB115R: NID-9634892: PIDN:CAA57056 1: PID:9534893 A.Genetics: A.Genetic	
Phenylalanine ammonia-lyase (PC 4.3.1.5) - carrot CJSpecies, Daucus carota (carrot) A.Filthe: Action specirum for induction of promotor activity of phenylalanine ammonia A.Filthe: Action specirum for induction of promotor activity of phenylalanine ammonia A.Filthe: Action specirum for induction of promotor activity of phenylalanine ammonia A.Filthe: Action specirum for induction of Davids (CJSpecial Color) A.Filther CJSpecial CJSpec	29 233 FAAAGVESGEFELJUPKESLALVNSTAVGSSMASKVLEDANVIALISEVLSALFAEVNOCK 292

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C:Keywords: ammonia-lyase; carbon-nitroqen lyase
F:201-203/Cross-link: 5-imidazollnone (Ala-Gly) *status predicted
F:202/Modified site: dehydroalanine (Ser) *status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: Phenylalanine ammonia-lyase gene structure, expression, and evolution in Nicot A;Reference number: S66343; MUID:96194455; PMID:8624404 A;Accession: S66343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Fukasawa-Akada, T.
Riol. 30,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             phenylalanine ammonia-lyase (EC 4.3.1.5) 1 - common tobacco
C:Species: Nicotiana tabacum (common tobacco)
C:Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29
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                                                                                                                                                                                                                                                                                                                                                                                         A; Gene: PAL1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-715 < FUK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A:Status: preliminary
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                                                                                                                                                         Matches
                                                                                                                                                                                                       Query Match
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  58
VSQVAGIAAANDS-DTVKVELSEAARAGVKASSDWVMESMNKGTDSYGVTTGFGATSHRR 116
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                                                   MASNGHVNGGENFELCKKSADPLNWEMAAESLRGSHLDEVKKMVSEFRKPMVKLGGESLT 60
                                                                                                 MENGNHVNGVVN-ELCIK--DPLNWGVAAEAL/TGSHLDEVKKMVAEFRKPVVKLGGETLI 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EELGRGFLTGEKVTSPGEEFDRVFTAMCKGQIIDPLLECLGGWNGEPLPI 710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ETEKNLSTSIFQKIAAFEDELKALLPKEVESARAVVESGNPAIPNRIKECRSYPLYKFIR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 \tt HKLKHHPGQIEAAAIMEHILDGSSYVKAAEKQHEMDPLQKPKQDRYALRTSPQWLGPQIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GFFELQPKEGLALVNGTAVGSGMASMVLFDANVLALLSEVLSAIFAEVMQGKPEFTDHLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ETEKNTNTSIFQKIATFEEELKVLLPKEVEGVRIAYENDT1,SIPNRIKACRSYPLYRFVR 660
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HKLKHHPGQIEAAAIMEYILDGSDYVKAAQKVHEMDPLQKPKQDRYALRTSPQWLGPQIE 360
                                                                                                                                                         610;
                                                                                                                                                                                  Similarity
                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T.; Kung, S.; Watson, J.C. 30, 711-722, 1996
                                                                                                                                                                            86.4%;
85.3%;
                                                                                                                                                       45;
                                                                                                                                                                                                       Score 3149;
                                                                                                                                                                            Pred.
                                                                                                                                                       Mismatches
                                                                                                                                                                                  No. 5.7e-194;
                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                     Length 715;
                                                                                                                                                    Indels
                                                                                                                                                    4.
                                                                                                                                                    Gaps
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A;Description: catalyzes the deamination of L-phenylalanine to trans-cinnamic acid A;Note: strongly induced during the hypersensitive reaction to TMV or to a fungal c;Superfamily: histidine ammonia-lyase C;Keywords: ammonia-lyase; carbon-nitrogen lyase C;Keywords: ammonia-lyase; carbon-nitrogen lyase F;198-200/Cross-link: 5-imidazolinone (Ala-Gly) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Title: Phenylalanine ammonia-lyase in tobacco. Molecular cloning and gene expressio A; Reference number: Z14995; MUID:95125127; PMID:7824656 A; Accession: T03663
                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-712 < PEL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R,Pellegrini, L.; Rohfritsch, O.; Fritig, B.; Legrand, M. Plant Physiol. 106, 877-886, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Nicotiana tabacum (common tobacco)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 16-Jul-1999
C;Accession: T03663
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                                                             F;199/Modified site: dehydroalanine (Ser) #status predicted
                                                                                                                                                                                                                                                       C; Function:
                                                                                                                                                                                                                                                                                       A; Gene: PAL
                                                                                                                                                                                                                                                                                                                     C; Genetics:
                                                                                                                                                                                                                                                                                                                                           A;Cross-references EMBL X78269; NID:g633596; PIDN:CAA55075.1, PID g633597
A;EXperimental source: cultivar Samsun NN; tissue-type leaves after infection by toba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        phenylalanine ammonia-lyase (EC 4.3.1.5) - common tobacco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T03663
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LMFAQFSELVNDFYNNGLPSNLSGGRNPSLDYGFKGGEIAMASYCSELQFLANPVTNHVQ 476
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LNNGETEKNTNTSIFOKIATFEEELKVLLPKEVEGVRIAYENDTLSIPNRIKACRSYPLY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QVAKKVLTMGVNGELHPSRFCEKDLLFVVDREYVFAYIDDVCSGTYPLMQKLRQVLVDHA 596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SAEQHNQDVNSLGLISARKTAEAVDILKLMSSTYLVALCQAIDLRHLEENLKNAVKNTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SAEQHNQDVNSI.GLTSARKTAEAVDII.KI.MSSTYLVAI.CQSIDI.RHI.EENMKSTVKNTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LMFAQFSELVNDYYNNGLFSNLTASRNFSLDYGFKGAEIAMASYCSELQFLANFVTNHVQ 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PQIEVIRAATKMLEREINSVNDNPLIDVSRNKALHGGNFQGTPIGVSMDNARLALASIGK
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   Score 3118.5;
Length 712;
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Matches Query Match

602;

Conservative

38;

Pred. No. Mismatches

5.2e-192; DB 2;

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Local Similarity

85.6%; 86.0%;

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phenylalanine ammonia lyase (EC 4.3.1.5) western baisam poplar x outtonwood Gryppetes. Populus trichorarpa x Populus deltoides (western baisam poplar x cottonwood) Grypate 30.5ept193 #sequence_revision 20.Aug 1994 #text_change 28-May-1999 GrAccession: J02265
                                                                                                                                     C:Superfamily histidine ammonia-lyase
C:Keywords: ammonia-lyase; carbon-nitrogen lyase
F;201-203/Cross-link: 5 imidazolinone (Ala Gly)
                                                                                                                                                                                                                      A,Cluss references: GB:L11747; NID:g169453; PIDN:AAA33805.1; PID:g169454
A;Note: the authors translated the codon AAG for residue 331 as GLu and AAG for residue
C;Comment: The enzyme plays a role in linking primary metabolism to phenylpropanoid meta-
                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                     A;Title: Structure, inheritance, and expression of hybrid poplar (Populus A;Reference number: JQ2265; MUID:94151434, FMID.8168506 A;Accession: JQ2265
                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Subramaniam, R.; Reinold, S.; Molitor, E.K.; Douglas, C.J. Plant Physiol. 102, 71-83, 1993
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                                                                                                      F; 202/Modified site: dehydroalanine (Ser) #status predicted
                                                                                                                                                                                                                                                                                                              A; Residues: 1-715 <SUB>
                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         613
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SARKTAFAVDII.KI.MSSTYI.VAI.CQSIDLRHI.EENMKSTVKNTVSQVAKKVI.TMGVNGEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DECYKYDPLNWEMAADSLKGSHLDEVKKMYAEFRKPYVKLGGETLTVAQVAATAAKDNAK 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ELCIK-DPLNWGVAAEALTGSHLDEVKKMVAEFRKPVVKLGGETLTVSQVAGIAAANDSD 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QKILAFEGELKAVLPKEVESARISLENGNPAIANRIKECRSYPLYRFVREELGAELLTGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ETINSVNDNPLIDVSRNKALHGGNFQGTPIGVSMDNARLALASIGKLMFAQFSELVNDYYN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAAIMEYILLGSDYVKAAQKVHEMDPLQKPKQDKYALKTSPQWLGPQIEVIRSSTKMIER 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALVNGTAVGSGLASMVLFDANILAVFSEVLSAIFAEVMNGKPEFTDHLTHKLKHHPGQIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TVKVELSEGARAGVKASSDWVMDSMSKGTDSYGVTTGFGATSHRRTKNGGALQKELIRFL 132
                                                                                                                                     imidazolinone (Ala Cly) #status predicted
                        85.5%;
84.1%;
Score 3116, Lp.,
No. 7.5e-192;
                                                Length, 715;
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A; Reference number: Z14446
A; Accession: T01858
A, Description, catalizes the deamination of L-phenylalanine to trans cinnamic acid C; Superfamily: histidine ammonia-lyase
                                                                                                                                                 C; Genetics:
                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-712 <T
                                                                                                                                                                                                                                                                                                                                                                                                                                 R.Taguchi, G.; Sharan, M.; Gonda, K.; Yanagisawa, K.; Shimosaka, M.; Hayashida,
J. Plant Biochem. and Biotech. 7, 79-84, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   phenylalanine ammonia-lyase (EC 4.3.1.5) - common talacco
C.Species: Nicotiana tabacum (common tabacco)
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                                                             C; Function:
                                                                                          A; Introns: 130/2
                                                                                                                    A;Gene: palA
                                                                                                                                                                              A; Experimental source: strain Bright Yellow; tissue type callus
                                                                                                                                                                                                            A; Cross-references: EMBL: AB008199; PIDN: BAA22947.1
                                                                                                                                                                                                                                                                                                      A, Status. preliminary, translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                              A:Title: Effect of methyl jasmonate and elicitor on PAL gene expression in tobacco ou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 599;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 QVAGIAAANDSDTVKVELSEAARAGVKASSDWVMESMNKGTDSYGVTTGFGATSHRRTKQ 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KRVLTTGANGELHPSRECHKELLKVVDREYVFAYVDDPCSATYPLMQKLRQVFVDHALEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AQFSELVNDFYNNGLPSNLTASRNPSLDYGFKGAEIAMASYCSELQYLANPVTTHVQSAE
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                                                                                                                                                                                                                                         1-712 <TAG>
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phenylalanine ammonia-lyase (EC 4.3.1.5) 1 - Lithospermum crythrorhizon (;Species: Lithospermum crythrorhizon C;Species: Lithospermum erythrorhizon C;Late: 09-Mar-1998 #sequence_revision 09-Mar-1998 #text_change 20-Jun-2000 C;Accession: JC5872; PC4506
R;Yazaki, K.; Kataoka, M.; Honda, G.; Severin, K.; Heide, L.
Biosci. Biotechnol. Biochem. 61, 1995-2003, 1997
A;Title. cDNA cloning and gene expression of phenylalanine ammonia-lyase in Lithospermum A;Reference number: JC5872, MUID 98101967; PMID:9438980
A;Accession: JC5872
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-710 <YAll>
                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 10
JC5872
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F;198-200/Cross-link, 5-imidazulinune (Ala Gly) #status predicted
F;199/Modified site: dehydroalanine (Ser) #status predicted
A;Residues: 1-710 <YAL>
A;Cross-references: DBBJ:D83075, NiD g2911121; PION:BAA24928 1; PID:g2911122
A;Accession: PC4506
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            613 QKILAFEDELKAVLPKEVESARAALESGNPAIANRIKECRSYPLYRFVRGELGAELLTGE 672
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KVRSPGEECDKVFTAMCNGQIIDSLLECLKEWNGAPLPIC 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HPSRFCEKDLLRVVDREYVFAYADDACSANYPLMQKLRQVLVDHALQNGENEKNANSSIF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALVNGTAVGSGMASMVLFDANVLALLSEVLSAIFAEVMQGKPEFTDHLTHKLKHHPGQIE 311
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86.1%; Pred. No. 1.9
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A:Molecule type: protein
A:Residucs: 348-479 'ARA'>
C:Comment: This enzyme catalyzes the first committed step in multibranched phenylprop
s of roots to protect them against pathogens in the soil
C:Superfamily: histidine ammonia-lyase
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660 EELGTELLTGEKVRSPGEELDKVFTAMCEGKLVDPLLACLEAWNGAPLPIC
                                                                                                               600 ENEKDYNTSIFHKIAIFEEELKAILPKEVENARASVENGIPAISNRIEECRSYPLYKFYR
                                                                                                                                                                                                                              540 RTLTTGVNGELHPSRFSEKDLLRVVDREYVFAYADDPCLTTYPLMQKLPETLVGHALDNG
                                                                                                                                                                                                                                                                                    541 KYLTMGVNGELHPSRFCEKDI.LRVVDREYVFAYIDDVCSGTYPLMQKLRQVI.VDHAI.NNG
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                                                      661 EELGRGFLTGEKVTSPGEEFDRVFTAMCKGQIIDPLLECLGGWNGEPLPIC 711
                                                                                                                                                                     601 ETEKNTNTSIFOKIATFERELKVLLPKEVEGVRIAYENDTLSIFNKIKACKSYFLYKFYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                420 QESELVNDYYNNGLPSNIJGSRNPSLDYGFKGAEIAMASYCSELQFLANPVTNHVQSAEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   421 QESELVNDFYNNGLESNI.SGGKNESLUYGEKGGELAMASYCSELQFLANPYTNHVQSAEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 HKLKHHEGQIEAAAIMEYILDGSDYVKAAQKVHEMDPLQKEKQDEYALETSEQWLGEQIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240 GFFELQPKEGLALVNGTAVGSGMASMVLYEANILAVLSEVISAIFAEVMNGKPEFTDHLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 GFFELQPKEGLALVNGTAVGSGMASMVLFDANVLALLSEVLSAIFAEVMQGKPEFTDHLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 I.NNNITPCLPIRGTITASGDLVPLSYIAGLLTGRPNSKAVGPTGEVLNAEKAFAAAGVEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 GALQKELIRFLNAGIFGNGTETSHTLPHSATRAAMLVRINTLLQGYSGIRFEILEAITKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 GALQKELIKFLNAGIFGNGTETSHTLPHSATRAAMIVRINTLLQGYSGIRFEILEAITKF 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 VAA1AARDDG---VTVELAEAAREGVKASSDWVMDSMNKGTDSYGVTTGFGATSHRRTKQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 VAGIAAANDSDTVKVELSEAAPAGVKASSDWVMESMNKGTDSYCVTTGPCATSHRRTKQC
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                                                                                                                                                                                                                                                                                                                                                 HNQDVNSLGLISSRKTSEAVEILKLMSSSFLVALFQAVDLRHIEENVRLAVKNTVSQVAK
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83.5%; Pred. No. 2.2e-189;
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phenylalanine ammonia-lyase (EC 4.3.1.5) - garden pea C:Species: Pisum sativum (garden pea) C:Tate: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 20-Jun-2000

C; Accession: S25303

RESULT 11

B;Kawamata, S.; Yamada, T.; Tanaka, Y.; Sriprasertsak, P.; Kato, H.; Ichinose, Y., Plant Mol. Biol. 20, 167-170, 1992
Plant Mol. Biol. 20, 167-170, 1992
A;Title: Molecular cloning of phenylalanine ammonia-lyase cDNA from Pisum sativum. A;Keference number, S25303, MUID:92385763; PMID:1515609

Ka

A; Accession:

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RESULT 12
S22991
S22991
S22991
Phenylalanine ammonia-lyase (PC 4.3.1.5) 1 - soybean
C:Species: Glycine max (soybean)
                                                                                                                                                                C:Date: 06-Jan-1994 *sequence_revision 10-Nov-1995 *text_change 16-Jul-1999
C:Accession: S22991
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                                          A;Title: Sequence and structure of a phenylalarine ammonia-lyase gene from Giycine max.
A;Reference number: $22991, MHTD 92190550, PMTD:1709682
                                                                                                       DNA Seq.
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A; Molecule type: DNA
                         A: Accession: S22991
                                                                                                                                   R; Frank, P L.;
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.Residues: 1·723 ∹KAW:-
                                                                                                                                                             Accession: $22991
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:209-211/Cross-link: 5 imidamolinone (Ala-Gly) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              615
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                                                                                                          1, 335-346, 1991
                                                                                                                                                                                                                                                                                                                                                                                    LGTGLLTGEKVISPGEECDKLFTAICQGKIIDPLLQCLCDWNGAPLPI 722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EKNLNTSIFQKIATFEDELKTLLPKEVESTRAAYESGNPTVPNKINGCRSYPLYRFVRQE 674
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LTTGVNGELHPSRFCEKDLLRVVDREHVFAYIDDPCSATYPLMQKLRQVLVDHALVNGES
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                                                                                                                                   Vodkin,
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83.9%;
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R;Lee, S.W.; Robb, J.; Nazar, R.N. J. Hibl Chem 267, 11824-11830, 1

C; Accession: A44133; S51076

A:Title: Truncated phenylalanine ammonia-lyase expression A;Reference number: A44133; MUID:92291052; PMID:1601854

II.

tomato (Lycopersicon

1992

phenylalanine ammonia-lyase (EC 4.3.1.5) - tomato C:Species Lyropersicon esculentum (tomato) C:Date: 10 Mar 1994 #sequence_revision 10 Mar 1994

#text_change

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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;200/Modified site: dehydroalanine (Ser) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Residues: 1-713 <FRA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Superfamily: histidine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best
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                                                   654 PLYKEVKERIGROFLIGEKVTSPGEEFIJKVFTAMCKGQTIJPILLEGIJGWNGEPLPT 710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              234 AAAGVEGGFFELQPKEGLALVNGTAVGSGMASMVLFDANVLALLSEVLSAIFAEVMQGKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            354 WLGPQIEVIRSSTKMIEREINSVNDNPLIDVSRNKALHGGNFQGTPIGVSMUNTRLAIAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.EA1TKFLNNNITPCLPLRGT1TASGDLVPLSY1AG1.LTGKPNSKAVGPTGEVLNAEKAF
                                                                                                                                                              DHALNNGETEKNINISIFQKIAIFEEEELKVLLPKEVEGVRIAYENDILSIPNRIKACRSY
                                                                                                                                                                                                                    TVSQVSKRILTTGVNGELHPSRFCEKDLLKVVDREYIFSYIDDFCSATYPLMQKLRQVLV 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HRRTKQGGALQKELIRFLNAGIFGNGTESSHTLPHTATFAAMLVFINTLLJGYSGIRFEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MENGN-HVNGVVNELCI-----KDPLNWGVAAEALTGSHLDEVKKMVAEERKPVVKLGG
                                                                                                           DHALVNAECEKDVNSSIEQKIAIEEEELKNILDKEVEGARAAYESGKAAIDNKIQECRSY 655
                                                                                                                                                                                                                                                                                                                       HVQSAEQHNQDVNSLGLISSRKTNEAIEILKLMSSTFLIALCQAIDLRHLEENLKNSVKN
                                                                                                                                                                                                                                                                                                                                                                                HVQSAEQHNQDVNSLGLISARKTAEAVDILKLMSSTYLVALCQSIDLRHLEENMKSTVKN 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WEGPLIEVIRESTKSTEREINSVNUNPLIEVSKNKALHGGNF QGIFFGVSMDNFKLALAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EFTDHLTHKLKHHPGQ1EAAA1MEY1LDGSDYVKAAQKVHEMDPLQKPKQDRYALRTSPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ELASINSEFFELQPKEGLALVNCTAVGSGLASMVLFEANILAVLSEVLSAIFAEVMOGKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ETLTIAQVAAVAGHDHG--VAVELSESAREGVKASSEWVMNSMNNGTDSYGVTTGFGATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ETLTVSQVAGIAAANDSDTVKVELSEAARAGVKASSDWVMESMNKGTDSYGVTTGFGATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEATINGHONG ---SECLSTAKGNNDPLNWGAAAEAMKGSHLDEVKRMVAEYRKPVVRLGG
PLYKFVREELGTGLLTGEKVKSPGEEFDKLFTAMCQGKIIDPLMECLGEWNGAPLPI 712
                                                                                                                                                                                                                                                                       TVSQVAKKVLTMGVNGELHPSRFCEKDLLRVVDRFYVFAY (DDVCSGTYPLMQKLRQVLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IGKEMEAQESEEVNDEYNNGEPSNESGGRNPSEDYGEKGGEIAMASYCSEEQFEANPVTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EFTDHLTHKLKHHPGQIEAAAIMEHILDGSSYMKAAKKLHEIDPLQKPKQDRYALRTSPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LEAITKILINNNYTPCLDLRGTITASGDLVPLSYLAGLLTGRPNSKAVGPSGEVLNAKEAF
                                                                                                                                                                                                                                                                                                                                                                                                                                   IGKLMFAQFSELVNDFYNNGLPSNLTASRNPSLDYGFKGAEIAMASYCSELQYLANPVTT
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A:Gene: PAL5
C;Superfamily: histidine ammonia-lyase
C;Keywords: ammonia-lyase; carbon-nitro
F;207-209/Cross-link: 5-imidazolinone (
F;208/Modified site: dehydroalanine (Se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A:Note sequence is inconsistent with the nucleotide translation A:Note: sequence extracted from NCB backbone (NCBIN:106680, NCBIP:106681) R:Lee, S.W.; Heinz, R.; Robb, J.; Nazar, R.N.

Eur. J. Blochem. 226, 109-114, 1994
A:Title: Differential utilization of alternate initiation sites in a plant defense gene A:Reference number: S51076; MUID:95045578; PMID:7957237
A:Accession: S51076
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A; Residues: 1-139 <LEW>
C; Genetics:
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-721 <LEE>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Keywords: ammonia-lyase; carbon-nitrogen lyase 207-209/Cross-link: 5-imidazolinone (Ala-Gly) **status predicted
665 LYRLYRQEVGTELLTGEKVRSPGEEIDKVFTAFCNGQIIDPLLECLKSWNGAPIPIC
                                                      655 LYRFVREELGRGFLTGEKVTSPGEEFDRVFTAMCKGQIIDPLLECLGGWNGEPLPIC 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   355 LGPQIEVIRSSTKMIEREINSVNDNPLIDVSRNKALHGGNFQGTPIGVSMDNTRLAIAAI 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  245 VAGVTSGFFELQPKEGLALVNGTAVGSGMASMYLFESNILAVMSEVLSAIFAEVMNGKPE 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        115 RRTKQGGALQKELIRFLNAGIFGNGTETSHTLPHSATRAAMIVRINTLLQGYSGIRFEIL 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65 LTVAQVASIANVDNKSNGVKVELSESARAGVKASSDWVMDSMGKGTDSYGVTTGFGATSH 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56 LTVSQVAGIA-AANDSDTVKVELSEAARAGVKASSDWVMESMNKGTDSYGVTTGFGATSH 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MENGNHVNGVVNELC-----IKDPLNWGVAAEALTGSHLDEVKKMVAEFRKPVVKLGGET 55
                                                                                                                                                                                                                                                                                               VSQVAKKVLTMGVNGELHPSRFCEKDLLRVVDREYVFAYIDDVCSGTYPLMQKLRQVLVD 594
                                                                                                                                                                                                                                                                                                                                                        VQSAEQHNQDVNSLGLISARKTAEAVDILKLMSSTYLVALCQAIDLRHLEENLKNAVKNT
                                                                                                                                                                                                                                                                                                                                                                                    VQSAEQHNQDVNSLGLISARKTAEAVDILKLMSSTYLVALCQSIDLRHLEENMKSTVKNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EATTKFLNNNITPCLPLRGTITASGDLVPLSYIAGLLTGRPNSKAVGPTGEVI.NAEKAFA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VQNG-HVNGEAMDLCKKSINVNDPLNWEMAAESLRGSHLDEVKKMVDEFRKPIVFLGGET 64
                                                                                                               HAMKNGESEKNLNSSIFQKIVAFEDELKAVLPKEVESARAVVESGNPAIPNKITECRSYP 664
                                                                                                                                                                         HALNNGETEKNTNTSIFOKIATFEEELKVLLPKEVEGVRIAYENDTLSIPNRIKACRSYP 654
                                                                                                                                                                                                                                  VSQVAKKTLAMGANGELHPARFCEKELLQVVEREYLFTYADDPCSSTYFLMQKLRQVLVD 604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GKLMFAQFSELVNDFYNNGLPSNLSGGRNPSLDYGFKGGEIAMASYCSELQFLANPVTNH 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LGPQIEVIRAATKMIEREINSVNDNPLIDVSRNKALHGGNFQGTPIGVSMDNTRLALASI
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83 0%; Pred No 9.8a
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C:Superfamily: histidine ammonia-lyase
C:Superfamily: histidine ammonia-lyase
C:Keywords: ammonia-lyase; carbon-nitrogen lyase
F:211-213/Cross-link: 5-imida.olinone (Ala-Gly) *status predicted
F:212/Modified site: dehydroalanine (Ser) *status predicted
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Plant Mol. Biol. 17, 415-429, 1991
A;Title: Stress responses in alfalfa (Medicago sativa L.). 12. Sequence analysis of p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:X58180; NID:g19649; PIDN:CAA41169.1; PID:g19650
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A; Residues: 1-725 <GOW>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nd developing plants
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
665 RGFLTGEKVTSPGEEFDRVFTAMCKGQIIDPLLECLGGWNGEPLPIC 711
                                                         619 NENTSIFÜKIATFEEELKTLLPKEVESARTAYESGNPTIPNKINGCRSYPLYKFVREELG
                                                                                                                   605 NTNTSIFQKIATFEEELKVLLPKEVEGVRIAYENDTLSIPNRIKACRSYPLYRFVREELG 664
                                                                                                                                                                                    559 MGVNGELHPSRFCEKDLLKVVDREHVFAYIDDPCSATYPLSQKLRQVLVDHALVNGESEK
                                                                                                                                                                                                                                                 545 MGVNGELHPSRFCEKDLLRVVDREYVFAYIDDVCSGTYPLMQKLRQVLVDHALNNGETEK 604
                                                                                                                                                                                                                                                                                                           499 VNSLGLISARKTNEAIEILQLMSSTFLIALCQAIDLRHLEENLKNSVKNTVSQVAKKTLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               425 LVNDFYNNGLPSNLSGGRNPSLDYGFKGGEIAMASYCSELQFLANPVTNHVQSAEQHNQD 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            379 STKSIEREINSVNDNPLIDVSRNKALHGGNFQGTPIGVSMDNTRLALASIGKLMFAQFSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         365 STKMIEREINSVNDNPLIDVSPNKALHGGNFQGTPIGVSMDNIPLAIAAIGKLMFAQESE 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   319 HHPGQIEAAAIMEHILDGSSYVKAAKKLHEIDPLQKPKQDKYALRTSPQWLGPLVEVIRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 245 LQPKEGLALVNGTAVGSGMASMVLFDANVLALLSEVLSAIFAEVMQGKPEFTDHLTHKLK 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                125 KELIRFLNAGIFGNGTETSHTLPHSATRAAMIVRINTLLQGYSGIRFEILEAITKFLNNN
                                                                                                                                                                                                                                                                                                                                                                        485 VNSLGLISARKTAEAVDILKLMSSTYIVALCQSIDLRHLEENMKSTVKNTVSQVAKKVLT 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        185 ITPCLPLRGTITASGDLVPLSYIAGLLTGRPNSKAVGPTGEVLNAEKAFAAAGVEGGFFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24 NNNNMKVNE---ADPLNWGVAAEAMKGSHLDEVKRMVAEYRKPVVRLGGETLTISQVAAI 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 NHVNGVVNELCIKDPLNWGVAAEALTGSHLDEVKKMVAEFRKPVVKLGGETLTVSQVAGI 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VTPCLPLRGTITASGDLVPLSYIAGLLTGRPNSKAHGPSGEVLNAKEAFNLAGINAEFFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAHDHG--VQVDLSESARDGVKASSEWVMESMNKGTDSYGVTTGFGATSHSRTKQGGALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                     LVNDFYNNGLPSNLSASRNPSLDYGFKGAEIAMASYCSELQYLANPVTTHVQSAEQHNQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HHPGQ1EAAAIMEY1LDGSDYVKAAQKVHEMDPLQKPKQDRYALRTSPQWLGPQ1EV1RS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 3067.5; DB 2
Pred. No. 9.9e-189;
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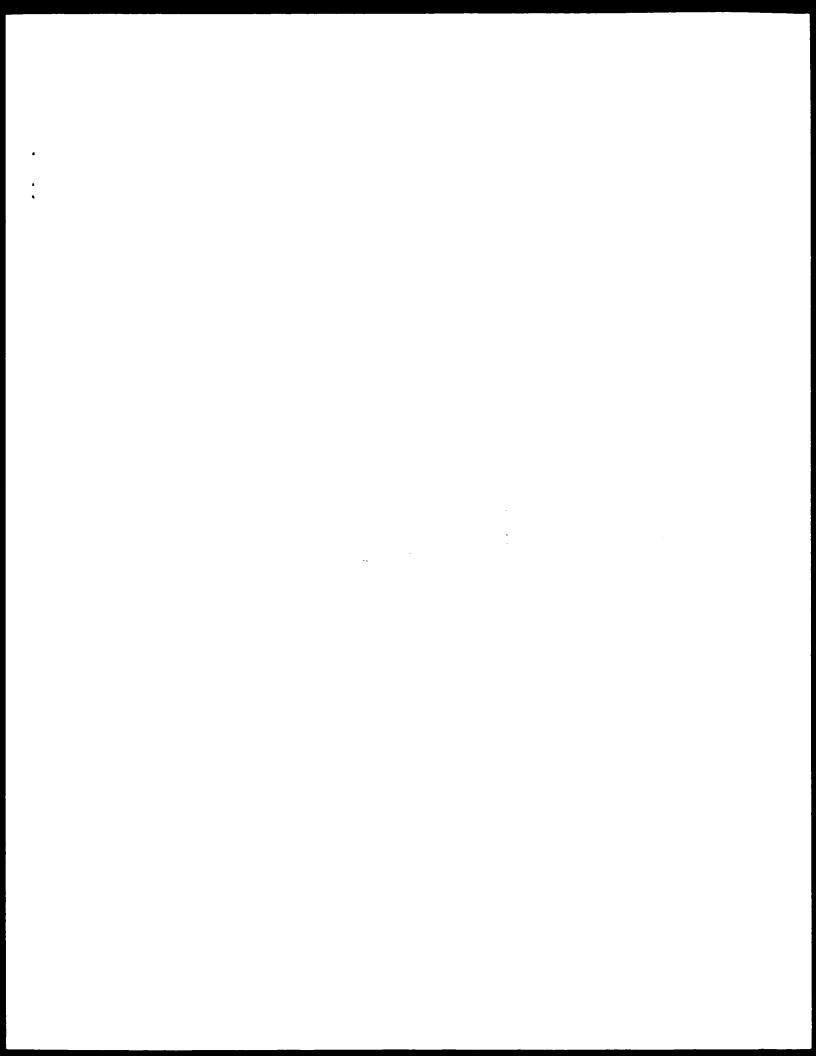
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RESULT 15
S04127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C:Superfamily: histidine ammonia-lyase
C:Keywords: ammonia-lyase; carbon nitrogen lyase
F:198-200/Cross-link: 5 imidazolinone (Ala-Cly) #status predicted
F:199/Modified site: dehydroalanine (Ser) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     phenylalanine ammonia-lyase (EC 4.3.1.5) class II - kidney bean C:Species: Phaseolus vulgaris (kidney bean) C:Species: Poseolus vulgaris (kidney bean) C:Date. 28:Feb-1990 #sequence_revision 28:Feb-1990 #text_change 21-May-1999 C:Accession: S04127 C:Accession: S04127 K:Cramer, C:L:: Edwards, K::Dron, M::Hang, X::Didino, S:L:: Holwell, G:Plant Mol.:Biol. 12, 367-383, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A:Title: Phenylalanine ammonia-lyase gene organization and structure. R:Releptence number: S04127
A:Accession: S04127
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Moslecule type: DNA
A:Residues: 1-712 <CRA>
C:Genetics:
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619 EEELKTLLPKEVEGARLAYENDQCAIPNKIKDCRSYPLYKFVREELGTSLLTGEKVISPG 678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            318 YILDGSUYVKAAQKVHEMDPLQKPKQDRYALKTSPQWLGPQIEVIRSSTKMIEREINSVN 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 259 AVGSGLASIVLFEANILAVLSEVISAIFAEVMQGKPEFTDHLTHKLKHHPGQIEAAAIME 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18 DPLNWGVAAEALTGSHLDEVKKMVAEFRKPVVKLGGETLTVSQVAGIAAANDSDTVKVEL 77
                            EMELKVLLPKEVEGVRIAYENDYLSIPNRIKACRSYPLYRFYREELGRGFLTGEKVTSPG 677
                                                                                                                                                                                                                                                                                                                                                      I.SGGRNPSIJDYGFKGGETAMASYCSELOFLANPVTNHVQSAFQHNQDVNSIGLISARKTA 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                            | DNPLIDVSRNKALHGGNFyGTF1GVSMDNTKLAIAA1GKLMFAQFSELVNDFYNNGLPSN 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEAARAGVKASSDWVMESMNKGTDSYGVTTGFGATSHRRTKQGGALQKELLRFLNAGIFG 137
                                                                                                                                                                                                              EALETEKLMSSTFLVALCQATDERHLEENEKNTVKNVVSQVAKRTETTGVNGELHPSRFC
                                                                                                                                                                                                                                                                                                                                                                                                                                DNPLISVSRNKALHGGNEGGTFIGVSMDNTRLAIASIGKLMFAGESDLVNDYYNNGLPSN 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HILDGSSYIKAAKKLHEIDPLOKPKODRYALRTSPOWLGPOIEVIRFSTKSIEREINSVN 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AVGSGMASMVLFDANVLALLSEVLSALFAEVMQGKPEFTDHLTHKLKHHPGQIEAAAIME 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NGTETSHTLPHSATRAAMIVRINTLLQGYSGIRFEILEAITKFLNNNITPCLPLRGTITA 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AESARACVKAISDWVMESMDKGTDSYGITTGFGATSHRRTKQGGALQKELIRFLNAGIFG 138
                                                                                                   EKALLKYVEREYTFAYIDDPCSGTYPLM©KLRÖVLVDYALANGENEKNLNTSIFQKIASF 618
                                                                                                                                                        EKDLLRVVDREYVFAYIDDVCSGTYPLMQKLRQVLVDHALNNGETEKNTNTSIFQKIATF 617
                                                                                                                                                                                                                                                                 EAVDILKLMSSTYLVALCQSIDLRHLEENMKSTVKNTVSQVAKKVLTMGVNGELHPSRFC 557
                                                                                                                                                                                                                                                                                                                       LTASRNPSLDYGFKGAEIAMASYCSELQYLANPVTSHVQSAEQHNQDVNSLGLISSRKTN 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SGDLVPLSYIAGLLTGRPNSKAVGPSGEILNAKEAFELANIGSEFFELQPKEGLALVNGT 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGDLVPLSYTAGLLTGRPNSKAVGPTGEVLNAEKAFAAAGVEGGFFELQPKEGLALVNGT 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NGTESNCTLPHTATRAAMLVRVNTLLQGYSGIRFELLEAITKILLNNNITPCLPLRGTITA 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           585; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 h 83.9%; Score 3058; DB 2; Similarity 84.3%; Pred. No. 3.9e-188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dron, M.; Liang, X., Dildino, S.L.; Bolwell, G.P.; Dixon,
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Search completed: March 29, Job time : 51 secs



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Minimum DB seq length: 0
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                              112892 seqs, 41476328 residues
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3644
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SUMMARIES
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• •			D.0		28 2994		30	141	(4)		22 3051		20 3067.5		18 3068 5			30			306	310	10 31	:43	311	143	315	5 3171	317	3 3185	$\alpha$	1 32	No. Score	D0011+
5 80.	5 80.	5 81.	5 81.	82	œ:	82.	83.	83.	83.	83.	51 83.7	83.	84.	84	84	84.	84.	84.		85.	85	85	85.	85.	8.5 85.6	85	86		87.	87.		06 88.ก	Match	01044
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PAL4_ARATH	PALI_RUBID	PAL1_IPOBA	FAL2_FOPKI	FAL2_IFOBA	PAL2_CICAR	PAL2_ARATH	PAL1_ARATH	FAL1_LYCES		FAL1_SOLTO	PAL2_LITER	PAI.2_PHAVU	PALY_MEDSA	PAL1_SOYBN	PALY_TRISU	PAL1_PEA	PALY_CITLI	PAL1_LITER	DALY_STYHU	PALY_DIGLA	PAL5_LYCES	PAL2_TOBAC	PAL1_PRUAV	PALY_POPTR	1 1	PAL1_TOBAC	PALY CAMSI	PAL1_DAUCA	PAL3_PETCR	PAL2_PETCR	PAL1_PETCR	FALY_HELAN	ID GI	
51	8 rubus id	ipomoea	Q43052 populus kit								lithosperm			_	4		7		N	023 <b>924 di</b> qitalis l	F26600 lycopersico			730 populus tr	5733	872 nicotiana	6 camell	865	729	œ	petr	≎04058 helianthus	Description	

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weery Match 88.98, Score 3206, EB 1, Length 667: Best Local Similarity 94.48; Pred. No. 1.4e-191; Matches 627; Conservative 13; Mismatches 24; Indels 0; Gaps

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1 MENGNHVNGVVNELCIKDPLNWGVAAEALTGSHLDEVKKMVAEERKDVVKLGGETLTVSQ 60

PO7218 phaseolus r	1 PALI_PHAVU	506	60.9	2220	5
P52777	1 PALY_PINTA	754	65.1	2373.5	44
P14717 r	1 PAL1_ORYSA	701	58.5	2500	3
Q40910 F	1 PAL4_POPKI	571	68.B	2506.5	42
P41426 solanum tub	1 PAL2_SOLTU	1065	909	Brsc	4
P45725 a	1 PAL3_ARATH	695	71.0	2585.5	40
P19143 phaseolus v	1 PAL3_PHAVU	710	71.1	2590	39
P53443 c	1 FAL2_ORYSA	710	72.2	2632.5	3 8
P45727 p	1 PALY_PERAE	620	73.3	2672.5	37
	1 PALY_WHEAT	700	74.9	2730.5	36
	1 PALY_BROF1	703	79.8	2908.5	S.
P45731 populus kit	1 PAL1_POPKI	682	79.8	2909	34

## ALIGNMENTS

RESULT 1
PALY_HELAN

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SEQUENCE 667 AA; 72076 MW; FBD3DB590EE70AB2 CRC64;	SQ
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TRACATAMS, LICROLARG, PRESAMELYASE) I.	7 5
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HSSP; P21310; 1B8F.	DR
EMBL, Y12461, CAA73065.1,	DR
of send an email to license@isb-sib.ch).	3 8
entities requires a license agreement (See http://www.isb-sib.ch/announce/	38
modified and this statement is not removed. Usage by and for commercial	cc
use by non-profit institutions as long as its content is in no way	cc.
The European Ricinformation Institute There are no restrictions on the	3 6
this Swiss-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioistormatics and the Ewar Latetation	3 6
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OF RESIDUES ALA-SER-GLY (BY SIMILARITY).	CC
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-!- PATHWAY: Phenylpropanoid biosynthesis; first step.	25
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(In) Plant Gene Register PGR98-108.	3.5
"Isolation of a complete PAL cDNA from sunflower.";	Ξ,
Tourvieille D., Ledoigt G.;	RA A
Mazeyrat F.A., Salles S., Drevet T., Roeckel-Drevet P.,	RA
SEQUENCE FROM N.A.	RP:
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NOBI TWACTOWARDS.	<b>?</b> ?
Asteridae; euasterids II; Asterales; Asteraceae; Asteroideae;	88
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;	00
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	00
Helianthus annuus (Common sunflower).	$^{\circ}$
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01-MAR-1992 (Rel. 21, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Phenylalanine ammonia-lyase 1 (EC 4.3.1.5).
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                                        SEQUENCE FROM N.A.
                                                                                                                                            cis-acting elements."
                                                                                                                                                                                  regulation and identification of elicitor and light responsive
                                                                                                                                                                                                               Lois R., Dietrich A., Hahlbrock K., Schulz W.;
"A phenylalanine ammonia-lyase gene from parsley: structure
                                                                                                                                                                                                                                                                                             MEDLINE=89356635;
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                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                               J. 8:1641-1648(1989).
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Logemann E.,
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"Serine-202 is the putative precursor of the active site dehydroalanine of phenylalanine ammonia lyase. Site-directed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lyase; Phenylpropanoid metabolism; Multigene family.

SITE 202 204 MODIFIED TO FORM 4-METHYLIDENE-IMIDAZOLE-
SITE 5-OME (BY SIMILARITY).

MUTAGEN 203 203 S->A: COMPLETE LOSS OF ACTIVITY.

MUTAGEN 210 210 S->A: NO LOSS OF ACTIVITY
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HSSP; P21310; 1B8F.
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PROSITE; PS00488; PAL_HISTIDASE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARIETY OF NATURAL PRODUCTS BASED ON THE PHENYLPROPANE SKELETON. CATALYTIC ACTIVITY: L-phenylalanine - trans-cinnamate + NH(3). PATHWAY: Phenylpropanoid biosynthesis; first step. SUBCELLULAR LOCATION: Cytoplasmic (Probable).

PTM: CONTAINS AN ACTIVE SITE 4-METHYLIDENE-IMIDAZOLE-5-ONE (MIO). PTM: CONTAINS AN ACTIVE SITE 4-METHYLIDENE-IMIDAZOLE-5-ONE (MIO). WHICH IS FORMED AUTOCATALYTICALLY BY CYCLIZATION AND DEHYDRATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO THE PAL / HISTIDASE FAMILY
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PEFTDHLTHKLKHHPGQIEAAAIMEHILDGSAYVKAAQKLHEMDPLQKPKQDRYALRTSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OF RESIDUES ALA-SER-GLY (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                             GETLTISQVAAI-SARDGSGVTVELSEAARAGVKASSDWVMDSMNKGTDSYGVTTGFGAT
                                       {\tt PEFTDHLTHKLKHHPGQIEAAAIMEYILDGSDYVKAAQKVHEMDPLQKPKQDRYALRTSP}
                                                                                    FKLAGVEGGFFELQPKEGLALVNGTAVGSGMASMVLFEANILAVLAEVMSAIFAEVMQGK
                                                                                                                            FAAAGVEGGFFELQPKEGLALVNGTAVGSGMASMVLFDANVLALLSEVLSAIFAEVMQGK 292
                                                                                                                                                                        1LEAITKFLNQNITPCLPLRGTITASGDLVPLSY1AGLLTGRPNSKAVGPTGV1LSPEEA
                                                                                                                                                                                                                ILEAITKFLNNNITPCLPLRGTITASGDLVPLSYIAGLLTGRPNSKAVGPTGEVLNAEKA
                                                                                                                                                                                                                                                        SHRRTKQGGALQKELIRFLNAGIFGNGSD--NTLPHSATKAAMLVRINTLLQGYSGIRFE
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210 S
77828 MW;
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86.2%;
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                                                                                                                                                                                                                                         the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Appert C., Logemann E., Hahlbrock K., Schmid J., Amrhein N.; "Structural and catalytic properties of the four phenylalanine ammonia-lyase isoenzymes from parsley (Petroselinum crispum Nym Eur J Blochem 225.491-499(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; cudicotyledons; core eudicots;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last amoutation update)
Phenylalanine ammonia-lyase 2 (EC 4.3.1.5).
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P45728;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Petroselinum crispum (Parsley) (Petroselinum hortense).
  Lyase, Fhenylpropanoid metabolism, Multigene family SITE 202 204 MODIFIED TO FORM 4-MET
                                       TIGREAMS; TIGRO1226; phe_am_lyase; PROSITE; PS00488; PAL_HISTIDASE; 1
                                                                                    InterPro; IPR001106; Phe/His_NH31yase
Plam; FF00221; PAL; 1
                                                                                                                                   EMBL; X81158, CAA57056.1;
HSSP; P21310; 188F.
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                                                                                                                                                                                                                                                                                                                                                                          PATHWAY: Phenylpropanoid biosynthesis; first step.
SUBCELLULAR LOWATION: Cynoplasmic (Probable)
PTM: CONTAINS AN ACTIVE SITE 4-METHYLDENE-MIDAZOLE-5-ONE (MIO)
WHICH IS FORMED AUTOCATALTTICALLY BY CYCLIZATION AND DEHYDRATION
OF RESIDUES ALA-SER-GLY (BY SIMILARITY).
SIMILARITY: HELONGS TO THE PAL / HISTIDASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: THIS IS A KEY ENZYME OF PLANT METABOLISM CATALYZING THE FURST REACTION IN THE BIOSYNTHESIS FROM I-PHENYLDALANINE OF A WIDE VARIETY OF MATURAL PRODUCTS BASED ON THE PHENYLDAPOPANE SKELFTON CATALYTIC ACTIVITY: I-phenylalanine - trans-cinnamate + NH(3).
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                                                                                                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through a collaboration -
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MODIFIED TO FORM 4-METHYLLDENE IMIDAZOLE
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YPLYKEVRKELGIEYLTGEKVTSPGEEFDKVFIAMSKGELLDPLLECLESWNGAPLPIC
                                                                                                 VEHALKNGDNERNMNTS (FQK (ATFEDELKALLPKEVESARAALESGNPA) PNR (EECRS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87.4%; Score 3185.5;
86.2%; Pred No 2 K
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RESULT 4

PALIS_PETCR

ID PALIS_PETCR

AC P45729;

III 01-NOV-1995 (Rei. 32, Created)

III 01-NOV-1995 (Pei. 32, Last sequence update)

DT 15-JIN-2002 (Pei. 32, Last sequence update)

DT 16-JIN-2002 (Pei. 32, Last sequence update)

DT 18-JIN 2002 (Pei. 32, Last sequence
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-!- FUNCTION: THIS IS A KEY ENZYME OF PLANT METABOLISM CATALYZING THE FIRST REACTION IN THE BIOSYNTHESIS FROM L-PHENYLALANINE OF A WIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGREAMS; TIGR01226; phe_am_lyase; 1.

PROSITE; PS00488; PAL_HISTIDASE; 1.

Lyase; Phenylpropanoid metabolism; Multigene family.

Lyase; Phenylpropanoid metabolism; Multigene family.

MODIFIED TO FORM 4-METHYLIDENE-IMIDAZOLE-

SITE

204

5-ONE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch)
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  487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180 FLNNNITFCLFLRGTITASGDLVPLSYIAGLLTGRPNSKAVGPTGEVLNAEKAFAAAGVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARIETY OF NATURAL PRODUCTS BASED ON THE PHENYLPROPANE SKELETON. CATALTYTC ACTIVITY: L-phenylalanine = trans-cinnamate + NH(3). PATHWAY: Phenylpropanoid biosynthesis; first step. SUBCELLULAR LOCATION: Cytoplasmic (Probable).

PTM: CONTAINS AN ACTIVE SITE 4-METHYLIDENE-IMIDAZOLE-5-ONE (MIO), WHICH IS FORMED AUTOCATALYTICALLY BY CYCLIZATION AND DEHYDRATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: BELONGS TO THE PAL / HISTIDASE FAMILY
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QHNQDVNSLGLISSRKTSEAVEILKLMSTTFLVGLCQAIDLRHLEENLKSTVKNTVSQVA
                                              QHNQDVNSLGLISARKTAEAVDILKLMSSTYLVALCQSIDLRHLEENMKSTVKNTVSQVA 539
                                                                                                                                                                                                EVIRSSTKM1EREINSVNDNPLIDVSRNKAIHGGNFQGSPIGVSMDNTRLAIAAIGKLMF
                                                                                                                                                                                                                                                                                                                                                 THKLKHHPGQIEAAAIMEYILDGSDYVKAAQKVHEMDPLQKPKQDRYALRTSPQWLGPQ1 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGFFELQPKEGLALVNGTAVGSGMASMVLFDANVLALLSEVLSAIFAEVMQGKPEFTDHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GALQKELIRFLNAGIFGNGTET-SHTLPHSATRAAMIVRINTLLQGYSGIRFEILEAITK 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VAGIAAANDSDTVKVELSEAARAGVKASSDWVMESMNKGTDSYGVTTGFGATSHRRTKQG 120
                                                                                                AQFSELVNDFYNNGLPSNLSGGRNPSLDYGFKGAETAMASYCSELQFLANPVTNHVQSAE
                                                                                                                                                                                                                                                 EVIRSSTKMIEREINSVNDNPLIDVSRNKALHGGNFQGTPIGVSMDNTRLAIAAIGKLMF
                                                                                                                                                                                                                                                                                                  THKLKHHPGQIEAAAIMEHILDGSAYVKAAQKLHEMDPLQKPKQDRYALRTSPQWLGPQI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GALQKELIRFLNAGIFGSGAEAGNNTLPHSATRAAMLVRINTLLQGYSGIRFEILEAITK 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VAAISARDDSG-VKVELSEEARAGVKASSDWVMDSMNKGTDSYGVTTGFGATSHRRTKQG
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                                                                                                                                              AQFSELVNDFYNNGLPSNLSGGRNPSLDYGFKGGEIAMASYCSELQFLANPVINHVQSAE
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87.1%; Pred. No. 7.7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Takeda J., Ozeki Y., Yoshida K.;
"Action spectrum for induction of promoter activity of phenylalanine ammonia-lyase gene by UV in carrot suspension cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              023865;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Phenylalanine ammonia-lyase 1 (EC 4.3.1.5).
                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                Lyase; Phenylpropanoid metabolism; Multigene family SITE 194 196 MODIFIED TO FORM 4-METI
                                                                                                                                                                                                 TIGRFAMS; TIGR01226; phe_am_lyase; 1. PROSITE; PS00488; PAL_HISTIDASE; 1.
                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Daucus carota (Carrot)
                                                                                                                                                                                                                                           Pfam; PF00221; PAL; 1
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                                                                                                                                                                                                                                                                                                   EMBL; D85850; BAA23367.1; -.
                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Photochem. Photobiol. 66:464-470(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97478956;
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                                                                                                                                                                                                                                                                nterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          547 KRVLTMGVNGELHPSRFCEKDLLRVVDREYIFAYIDDPCSATYPLMQKLRETLVEHALNN
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2 ENGNHVNGVVNELCI-KDPLNWGVAAEALTGSHLDEVKKMVAEFRKPVVKLGGETLTVSQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CATALYTIC ACTIVITY: L-phenylalanine = trans-cinnamate + NH(3). PATHMAY: Phenylpropanoid biosynthesis; first step. SUBCELLULAR LOCATION: Cytoplasmic (Probale). PTM: CONTAINS AN ACTIVE SITE 4-METHYLIDENE-IMIDAZOLE-5-ONE (MIO). WHICH IS FORMED AUTOCATALYTICALLY BY CYCLIZATION AND DEHYDRATION OF RESIDUES ALA-SER-GLY (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: THIS IS A KEY ENZYME OF PLANT METABOLISM CATALYZING TO FIRST REACTION IN THE BIOSYNTHESIS FROM L-PHENYLALANINE OF A WILL ARIETY OF NATURAL PRODUCTS BASED ON THE PHENYLPROPANE SKELETON THE PHENYLPROPANE SKELETON
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                                                          Similarity
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                                                                                                                    708 AA;
                                       Conservative
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                                                        87.0%;
87.2%;
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                                     41; Mismatches
                                                                             Score 3171.5;
                                                          Pred.
                                                                                                                    5-ONE (BY SIMILARITY).; 0610411373E680E3 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta, Trachee
Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; Ericales; Theaceae; Camellia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Phenylalanine ammonia-lyase (EC 4.3.1.5).
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P45726;
                                                                                                                                                                           "Molecular cloning of phenylalanine ammonia-lyase cDNA and classification of varieties and cultivars of tea plants (Camellia sinensis) using the Lea PAL cDNA probe.";
Theor Appl. Genet 89 671-675(1994)
                                                                                                                                                                                                                                                                                                                 STRAIN-CV. Ya
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                FUNCTION: THIS IS A KEY ENZYME OF PLANT METABOLISM CATALYZING THE FIRST REACTION IN THE BIOSYNTHESIS FROM I.-PHENYLALANINE OF A WID VARIETY OF NATURAL PRODUCTS HASBE ON THE PHENYLPODANE SKELETON. CATALYTIC ACTIVITY: L-phenylalanine - Lrans-cinnamate + NH(3).
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Takeuchi A., Hayatsu M., Kondo S.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no restrictions on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the Swiss Institute of Bioinformatics and the Swiss Institute of Bioinformatics.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; D26596; BAA05643.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001106; Phe/His_NH31yase.
    606
                                                                                                   543 LTMSVNGELHPSPFCEKDLLFVVDKEYVFAYIDDVCSGTYPLMQKLFQVLVCHALNNGET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     123 LQKELIRFLNAGIFGNGTETSHTLPHSATPAAMIVRINTLL/20YSGTPFEILEAITKFLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68 AIAVRGSE--VAVELSESAREGVKASSDWVMESMNKGTDSYGVTTGFGATSHRRTKEGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 GNGVGSGGSPGFCLKDPLNWGVAAEAMKGSHLEEVKGMVEEFRKPVVRLGGETLTISQVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 GNHV-NGVVNELCIKDPLNWGVAAEALTGSHLDEVKKMVAEFRKFVVKLGGETLTVSQVA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Cytoplasmic (Probable).
PTM: CONTAINS AN ACTIVE SITE 4-METHYLIDENE-IMIDAZOLE-5-ONE (MIO).
WHICH IS FORMED AUTOCATALYTICALLY BY CYCLIZATION AND DEHYDRATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OF RESIDUES ALA-SER-GLY (BY SIMILARITY).
SIMILARITY: BELONGS TO THE PAL / HISTIDASE FAMILY.
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                                                                                                                                                                                                        QDVNSLGLISARKTAEAVDILKLMSSTYLVALCQSIDLRHLEENMKSTVKNTVSQVAKKV
                                                                                                                                                                                                                                                                                                                                                         PSSTKMIEREINSVNONPLICVSPNKALHGGNEGGTPIGVSMCNTFLAIAANIGKLMFAQF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FELQPKEGLALVNGTAVGSGLASMVLFEANILAVLSEVLSA1FAEVMQGKPEFTDHLTHK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FELQPKEGLALVNGTAVGSGMASMVLFDANVLALLSEVLSATFAEVMQGKPEFTDHLTHK
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EKNLSTSIFQKIRAFEEEIKTLLPKEVESTRAAIENGNSAIPNRIKECRSYPLYKFVREE
                                      EKNTNTSTEOKTATEEEELKVLLPKEVEGVRTAYENDTLSTPNRTKACRSYPLYREVREE
                                                                               LTMGVNGELHESKECEKULLRVVDREYIFAYIDDECSATYELMQKLRQVLVEHALKNGES
                                                                                                                                                               QDVNSLGLISSRKTAEAVDILKLMSSTYLVALCQAVDLRHFEENLRNTVKSTVSQVAKKV
                                                                                                                                                                                                                                               SELVNDFYNNGLPSNLSGGRNPSLDYGFKGAEIAMAAYCSELQFLANPYTNHVQSAEQHN
                                                                                                                                                                                                                                                                                        SELVNUFYNNGLPSNI.SGGKNPSLDYGFKGGETAMASYCSELOFT.ANPVTNHVOSAEOHN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 3154 5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MODIFIED TO FORM 4 METHYLIDENE IMIDAZOLE - 5-ONE (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.4e-188;
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Best Local
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PROSITE: PS00488; PALL HISTIDASE; 1.
Lyase; Phenylpropanoid metabolism; Multigene family.
Lyase; Phenylpropanoid metabolism; Multigene family.
MODIFIED TO FORM 4-METH
SITE 201 203 5-ONE (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Taguchi G., Sharan M., Gonda K., Yanagisawa K., Shimosaka M., Hayashida N., Okazaki M.; Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THIS IS A KEY ENZYME OF PLANT METABOLISM CATALYZING FIRST REACTION IN THE BIOSYNTHESIS FROM L-PHENYLALANINE OF A W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nicotiana tabacum (Common tobacco).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Maynoliophyta; eudicotyjedons; core eudicots;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PALI_TOBAC STANDARD; PRT; 715 AA P25872; 01-MAY-1992 (Rcl. 22, Created) 01-MAY-1992 (Rcl. 22, Last sequence update) 15-JUN-2002 (Rcl. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             _TOBAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Phenylanine ammonia-lyase (EC 4.3.1.5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. Th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=cv. Bright Yellow; TISSUE=Callus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (XXX-1992) to the EMBL/GenBank/DDBJ databases
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       117
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                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                1 MENGNHVNGVVN-ELCIK--DPLNWGVAAEALTGSHLDEVKKMVAEFRKPVVKLGGETLT 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PATHWAY: Phenylpropanoid biosynthesis; first step.
SUBCELLULAR LOCATION: Cytoplasmic (Probable).
PTM: CONTAINS AN ACTIVE SITE 4-METHYLIDENE-IMIDAZOLE-5-ONE (MIO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARIETY OF NATURAL PRODUCTS BASED ON THE PHENYLPROPANE SKELETON CATALYTIC ACTIVITY: L-phenylalanine - trans-cinnamate + NH(3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE PAL / HISTIDASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WHICH IS FORMED AUTOCATALYTICALLY BY CYCLIZATION AND DEHYDRATION OF RESIDUES ALA-SER-GLY (BY SIMILARITY).
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                                                                    VAQVAATAVRDKSANGVKVELSEEARAGVKASSDWVMDSMNKGTDSYGVTTGFGATSHRR 120
                                                                                                                                      VSQVAGIAAANDS-DTVKVELSEAARAGVKASSDWVMESMNKGTDSYGVTTGFGATSHRR 116
                                                                                                                                                                                                       MASNGHVNGGENFELCKKSADPLNWEMAAESLRGSHLDEVKKMVSEFRKPMVKLGGESLT
   TKQGGALQKELIFFLNAGIFGNGTETSHTLPHSATRAAMIVFINTLLQGYSGIFFEILEA 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AB008200; BA
P21310; 1B8F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       715 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       77780 MW;
                                                                                                                                                                                                                                                                                                                                                                                 86.4%; Score 3149; DB 1; 85.3%; Pred. No. 5.2e-188
                                                                                                                                                                                                                                                                                                                                                    45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MODIFIED TO FORM 4-METHYLIDENE-IMIDAZOLE-5-ONE (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOY-1995 (Rel. 32, Created)
01-NOY-1995 (Rel. 32, Last sequence update)
15-UUN-2002 (Rel. 41, Last annotation update)
Phenylalanine ammonia-lyase (EC 4.3.1.5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PAL3_TO P45733;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOBAC
                                                                                                                                                                                         expression during the hypersensitive reaction to tobacco mosaic virus and the response to a fungal elicitor."; plant physiol. 106:897-886(1994).
-i- FUNCTION: THIS IS A KEY ENZYME OF PLANT METABOLISM CATALYZING THE FIRST REACTION IN THE BIOSYNTHESIS FROM L-PHENYLALANINE OF A WIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta, Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids 1; Solanales; Solanaceae; Nicotiana.
                                                                                                                                                                                                                                                                                                                                                 STRAIN=cv. Samsun NN; TISSUE=Leaf; MEDLINE=95125127; PubMed=7824656;
                                                                                                                                                                                                                                                                                                     Peilegrini L., Rohfritsch O., Fritig B., Legrand M., "Phenylalanine ammonia-lyase in tobacco. Molecular cloning and gene
                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=4097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nicotiana tabacum (Common tobacco)
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                     VARIETY OF NATURAL PRODUCTS BASED ON THE PHENYLPROPANE SKELETON. CATALITIC ACTIVITY. L-phenylalanine = trans-cianamate + NH(3). PATHMAY: Phenylpropanoid blosynthesis; first step. SUBCELLULAR LOCATION: Cytoplasmic (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            _TOBAC
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TMY OR TO A FUNGAL ELICITOR.

PTM: CONTAINS AN ACTIVE SITE 4-METHYLLDENE-IMIDAZOLE-5-ONE (MIO) WHICH IS EVEMED AUTOCATALYTICALLY BY CYCLIZATION AND DEHYDRATION

OF RESIDUES ALA-SER-GLY (BY SIMILARITY).

INDUCTION: STRONGLY INDUCED DURING THE HYPERSENSITIVE REACTION TO

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long modified and this statement is not removed
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HSSP; P21310; IB8F.
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                                                                                  QKILAFEGELKAVLPKEVESARISLENGNPAIANPIKEGPSYPLYRFVPEELGAELLTGE 672
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                                                                                                                                                                                                                                                           SARKTAEAVDILKLMSSTYLVALCQAIDLRHLEENLRNAVKNTVSQVAKRTLTMGANGEL 552
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                                      KVTSPGEHEDRVFTAMCKGQIIDPLLECLGGWNGEPLPIC 711
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PALY_POPTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    trichocarpa x Populus deltoides) phenylalanine ammonia-lyase genes.";
Plant Physiol. 102:71-83(1993).
-i- FUNCTION: THIS IS A KEY ENZYME OF PLANT METABOLISM CATALYZING THE
FIRST REACTION IN THE BIOSYNTHESIS FROM L-PHENYLALANINE OF A WIDE
VARIETY OF NATURAL PRODUCTS BASED ON THE PHENYLPPOPANE SKELETON.
-i- CATALYTIC ACTIVITY: L-Phenylalanine - trans-cinnamate (NH(3)).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta; Spermatophyta: Magnoliophyta; eudicotyledons; core eudicots; Rosid eurosids I, Malpighiales; Salicaceae; Populus.
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15-TUN-2002 (Pel. 41, Last annotation update)
Phenylalanine ammonia-lyase (EC 4.3.1.5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN*P.trichocarpa X P.deltoides; TISSUE*Leaf; MEDLINE-94151434; PubMed-8108506;
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01-NOV-1995 (Rel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIGREAMS; TIGRO1226; phe_am_lyase; 1. PROSITE; PSO0488; PAL_HISTIDASE; 1
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HSSP; F21310; 1B8F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROLE-OITY is expyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Subramaniam R , Reinold S , Molitor E K , Douglas C.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Populus trichocarpa (Western balsam poplar)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lyase; Phenylpropanoid metabolism; Multigene family SITE 201 203 MÖDIFIED TO FORM 4-MET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00221; PAL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb/sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCHI_TaxID=3694;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no restrictions on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Structure, inheritance, and expression of hybrid poplar (Populus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
184 LLNNNITPCLPLRGTITASGDLVPLSYIAGLLTGPPNSKATGPTGEVLDAAEAFKAAGIE
                                                                                                         120 - FALQKELIFFLNAGIFGNGTETSHTLPHSATRAAMIVRINTLLQGYSGIRFEILEAITK 179
                                           180 FENNNLEPCEPERGITEASGDLVPESYTAGELIIGRPNSKAVGPIGEVENAEKAFAAAGVE 239
                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                          65 QVAST-AGHDTGDVKVELSESARPGVKASSDWVMDSMDKGTDSYGVTTGFGATSHRRTKQ
                                                                                                                                                                                                                 60 QVAGIAAANDSDTVKVELSEAAPAGVKASSDWVMESMNKGIDSYGVIIGFGATSHPRIKO 119
                                                                                                                                                                                                                                                             6 KNG-YQNGSLESIA'VNQRDPLSWGVAAEAMKGSHLDEVKRMVADYRKPVVKLGGETLTIA 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PATHWAY: Phenylpropanoid biosynthesis; first step.
SUBCELLULAR LOCATION: Cytoplasmic (Probable).
PTM - CONTAINS AN ACTIVE SITE 4 METHYLIPARE-IMIDAZOLE-5 ONE (MIO).
WHICH IS FORMED AUTOCATALYTICALLY BY CYCLIZATION AND DEHYDRATION
                                                                                                                                                                                                                                                                                                      2 ENGNHVNGVVNELCI -- KDPLNWGVAAEALIGSHLDEVKKMVAEEKKPVVNLGGETLTVS
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                                                                                     GGALQKELIRFLNAGIFGNGTETCHTLPHSATRAMLVRINTLLQGYSGIRFEILEAITK
                                                                                                                                                                                                                                                                                                                                                    599;
                                                                                                                                                                                                                                                                                                                                                                       h 85.5%; Score 3116;
Similarity 84 1%; Pred. No. 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR001106; Phe/His_NH31yase.
                                                                                                                                                                                                                                                                                                                                                                                                                                          715 AA;
                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          77918 MW;
                                                                                                                                                                                                                                                                                                                                                    26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MODIFIED TO FORM 4-METHYLIDENE-IMIDAZOLE-5-ONE (HY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                          589E837A6E8AF2H6 CRC64;
                                                                                                                                                                                                                                                                                                                                                  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                       5.8e-186;
                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
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                                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.ish-sib ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "A full-length cDNA for phenylalanine ammonia-lyase cloned from ripe Sweet Cherry fruit (Prunus avium).";
(In) Plant Gene Register PGR98-184.
-!- PUNCTION: THIS IS A KEY ENZYME OF PLANT METABOLISM CATALYZING THE FIRST REACTION IN THE HIGSYNTHESIS FROM L-PHENYLALANINE OF A WIDE VARIETY OF NATURAL PRODUCTS BASED ON THE PHBYLLPROPANE SKELEFON.
-!- CATALYTIC ACTIVITY: L-phenylalanine - trans-cinnamate + NH(3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PALL_PRUAV STANDARD; PRT; 717 AA. 064963; 30-MAY-2000 (Rel. 39, Created) 30-MAY-2000 (Rel. 39, Last sequence update) 15-JIN-2002 (Rel. 41, Last annotation update) Phenylalanine ammonia-lyase 1 (EC 4.3.1.5).
                                                                                                                                                                                                                                                This
or send an email to license@isb-sib.ch)
                                                                                                                                                              the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-CV.
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                                                                                                                                                                                                         between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=42229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Prunus avium (Cherry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    664
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                                                                                                                                                                                                                                                                                                                                                                                                                                         PATHWAY: Phenylpropanoid biosynthesis; first step.
SUBCELLULAR LOCATION: Cytoplasmic (Probable).
PTM: CONTAINS AN ACTIVE SITE 4-METHYLLDENE-IMIDAZOLE-5-ONE (MIO)
                                                                                                                                                                                                                                                                                                                         OF RESIDUES ALA-SER-GLY (BY SIMILARITY). SIMILARITY: BELONGS TO THE PAL / HISTIDASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                        WHICH IS FORMED AUTOCATALYTICALLY BY CYCLIZATION AND DEHYDRATION OF RESIDUES ALA-SER-GLY FRY STATIANTON
                                                                                                                                                      SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
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PAL2_TOBAC STANDARD; PRT; 7 P35513; 022114; 01-JUN-1994 (Rel. 29, Created) 15-JUL-1998 (Rel. 36, Last sequence up 15-JUN-2002 (Rel. 41, Last annotation

update)

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Phenylalanine ammonia-lyase (EC 4.3.1.5).

PAL2_TOBAC

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Best Local
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SITE 203 205 MODIFIED TO FORM 4-METHYLIDENE-IMIDAZOLE-
5-ONE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00221; PAL; 1.
TIGRFAMS; TIGR01226; phe_am_lyase; 1.
PROS(TE; PS00488; PAL_HISTIDASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, AF036948; AAC78457.1; HSSP; P21310; 1B8F.
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665 VREELGAEYLTGEKVRSPGEECDKVFTAICEGKIIDPILDCLEGWNGAPLPIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 QNG-HKNGSVELPELCIKKOPLNWGVAAFTLKGSHLDEVKRMVAEYRKPVVKLGGESLTI 66
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                                                                          VREELGRGFLTGEKVTSPGEEFDRVFTAMCKGQIIDPLLECLGGWNGEPLPIC
                                                                                                                                                                      NGENEKNASTSIFQKIVAFEEELKVLLPKEVDSARAALDSGSAGVPNRITECRSYPLYKF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00488; PAL_HISTIDASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hayashida N., Okazaki M.;
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Cloning and sequencing of a full length cDNA coding for phenylalanine ammonia-lyase from tobacco cell culture."; plant Physiol. 104\cdot1001\cdot1002(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nicoliana tabacum (Common tobacco)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots;
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb/sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Taguchi G , Sharan M ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (OCT-1997) to the EMBL/GenBank/DUBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nagai
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nagai N., Kitauchi H., Shimosaka M., Okazaki M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=94218401; PubMed-8165251,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID-4097
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lyase; Phenylpropanoid metabolism; Multigene family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ptam; PF00221; PAL; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001106; Phe/His_NH31yasc
193 RGTITASGDLVPLSYTAGLLTGPPNSKAVGPNGETLNAEEAFRVAGVNGGFFELQPKEGL
                                          192
                                                                                                                                                                                                                                             13 DFCMKVDPLNWEMAADSLKGSHLDEVKKMVAEFRKPVVKLGGETLTVAQVAAIAAKDNVK 72
                                                                                                                                                                                                                                                                                  13 ELCIK-DPLNWGVAAEALTGSHLDEVKKMYAEFRKPVVKLGGETLTVSQVAGIAAANDSD 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: THIS IS A KEY ENZYME OF PLÂNI METABOLISM CATALYZING THE FIRST REACTION IN THE BIOSYNTHESIS FROM L-PHEMYLALANINE OF A WIDE VARIETY OF NATURAL PRODUCTS HASED ON THE PHEMYLAPPOPANE SKELETON CATALYTIC ACTIVITY: L-phenylalanine = Lrans-cinnamate + NH(3). PATHWAY: Phenylpropancid binsynthesis, first stop SUBCELLULAR LOCATION: CYTOplasmic (Probable).

SUBCELLULAR LOCATION: CYTOplasmic (Probable).

PTM: CONTAINS AN ACTIVE SITE 4-METHYLIPPME-IMIDAZOLE-S-ONE (M:O), WHICH IS FORMED AUTOCATALYTICALLY MY CYCLIZATION AND DEHYDRATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OF RESIDUES ALA-SER-GLY (BY SIMILARITY).
SIMILARITY: BELONGS TO THE PAL / HISTIDASE FAMILY
                                                                                                                                                              TVKVELSEGARAGVKASSDWVMDSMGKGTDSYGVTTGEGATSHRRTKNGGALQKELIRFL 132
                                                                                                                        NAGIFGNGTETSHTLPHSATRAAMIVRINTLLQGYSGIRFEILEAITKFLNNNITPCLPL 191
                                                                                                                                                                                                     TVKVELSEAARAGVKASSDWVMESMNKGTDSYGVTTGFGATSHPPTKQGGALQKELIPFL 131
                                      RCTITASGDLVPLSYIAGLLTGRPNSKAVCPTCEVLNAEKAFAAACVECCFFELQPKECL 251
                                                                             NAGVEGNGTESCHTLPQSGTRAAMLVRINILLQGYSGIRFEILEAIIKLLNHNVTPCLPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AB008199;
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                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                              712 AA;
                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                       198
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                                                                                                                                                                                                                                                                                                                                                                                                              77345 MW;
                                                                                                                                                                                                                                                                                                                                                85 3%; Score 3109 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gonda K , Yanaqisawa K , Shimosaka M.
                                                                                                                                                                                                                                                                                                                             35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                         MODIFIED TO FORM 4-METHYLIDENE-IMIDAZOLE-5-ONE (HY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                  Pred No 1 5e-1
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                                                                                                                                                                                                                                                                                                                             61, Indels
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PAL5_LYCES
            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb/sib.ch/announce/
                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=cv. Bonny Best;
MEDLINE-92291052; PubMed-1601854;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUN-2002 (Ref. 41, Last annotation update) 
Phenylalanine ammonia-lyase (BC 4 3 1.5) (PAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-AUG-1992 (Rei. 23, Last sequence update)
15-JUN-2002 (Rei. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Spermatophyta; Magnoliophyta; endicotyledons; core endicots;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-AUG-1992 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                     (Lycopersicon esculentum).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Truncated phenylalanine ammonia lyase expression in tomato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCHI_TaxID~4081;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lycopersicon esculentum (Tomato)
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                                                                                                                                                                           WHICH IS FORMED AUTOCATALYTICALLY BY CYCLIZATION AND DEHYDRATION OF RESIDUES ALA-SER-GLY (BY SIMILARITY).
SIMILARITY: BELONGS TO THE PAL / HISTIDASE FAMILY.
                                                                                                                                                                                                                                                  PATHWAY: Phenylpropanoid biosynthesis; first step.
SUBCELLULAR LOCATION: Cytoplasmic (Probable).
PIM: CONTAINS AN ACTIVE SITE 4-METHYLIDENE IMIDAEOLE-5-ONE (MIO).
                                                                                                                                                                                                                                                                                                                  BIOL. Chem. 267:11824-11839(1992).

FUNCTION: THIS IS A KEY ENZYMI OF PLANT METABOLISM CATALYZING THE FUNCTION. ITHE SIS A KEY ENZYMIHESIS FROM L-PHENYLALANINE OF A WIDE VARIETY OF NATURAL PRODUCTS BASED ON THE PHENYLPROPANE SKELETON. CATALYTIC ACTIVITY: L-phonylalanine - trans-cinnamate · NH(3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KVRSPGEECDKVFTAMCNGQIIDSLLECLKEWNGAPLPIC 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KYTSPGPTEDMYFTAMCKGQ1;DPLLECLGGWNGEPLP1C 711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HPSRECEKDIJJRVVDREYVFAYADDACSANYPIMQKIRQVIVDHALQNGENEKNANSSIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SARKTAEAVDILKIMSSTYLVALCQSIDLRHLEENMKSTVKNIVSQVAKKVLIMGVNGEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NGLESNLTAGKNESLDYGEKGSETAMASYCSELQFLANEVTNHVQSAEQHNQDVNSLDLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QKIATFEEELKVLLPKEVEGYPIAYENDTLSIPNPIKACESYPLYRFVREELGRGFLTGE
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RESULT 13
PALY_DIGLA
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DE Phenyl
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Best Local
023924;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Phenylalanine ammonia-lyase (EC 4.3.1.5).
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                                                                                                                                         PALY_DIGLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lyase; Phenylpropanoid metabolism; Multigene family
                                                                                                                                                                                                                                              665 LYRLVRQEVGTELLTGEKVRSPGEEIDKVFTAFCNGQIIDPLLECLKSWNGAPIPIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       485
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                                                                                                                                                                                                                                                                                            LYRFVREELGRGFLTGEKVTSPGEEFDRVFTAMCKGQIIDPLLECLGGWNGEPLPIC 711
                                                                                                                                                                                                                                                                                                                                                                                 HALNNGETEKNTNTSIFQKIATFEEELKVLLPKEVEGVRIAYENDTLSIPNRIKACRSYP 654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GKLMFAQFSELVNDYYNNGLPLNLTAGRNPSLDYGLKGAEIAMASYCSELQFLANPVTNH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GKLMFAQFSELVNDFYNNGLPSNLSGGRNPSLDYGFKGGEIAMASYCSELQFLANPVTNH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VAGVTSGFFELQPKEGLALVNGTAVGSGMASMVLFESNILAVMSEVLSAIFAEVMNGKPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LTVAQVASIANVDNKSNGVKVELSESARAGVKASSDWVMDSMGKGTDSYGVTTGFGATSH 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LTVSQVAGIA-AANDSDTVKVELSEAARAGVKASSDWVMESMNKGTDSYGVTTGFGATSH 114
                                                                                                                                                                                                                                                                                                                                        HAMKNGESEKNLNSSIFQKIVAFEDELKAVLPKEVESARAVVESGNPAIPNRITECRSYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VSQVAKKVLTMGVNGELHESRFCEKDLLRVVDREYVFAY1DDVCSGTYPLMQKLRQVLVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VQSAEQHNQDVNSLGLISARKTAEAVDILKLMSSTYLVALCQAIDLRHLEENLKNAVKNT 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VQSAEQHNQDVNSLGLISARKTAEAVDILKLMSSTYLVALCQSIDLRHLEENMKSTVKNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LGPQIEVIRAATKMIEREINSVNDNPLIDVSRNKALHGGNFQGTPIGVSMDNTRLALASI 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 {\tt FTDYLTHKLKHHPGQIEAAAIMEHILDGSSYVKAAQKLHEMDPLQKPKQDRYALRISPQW}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VQNG-HVNGEAMDLCKKSINVNDPLNWEMAAESLRGSHLDEVKKMVDEFRKPIVKLGGET 64
                                                                                                                                                                                                                                                                                                                                                                                                                               VSQVAKKTLAMGANGELHPARFCEKELLQVVEREYLFTYADDPCSSTYPLMQKLRQVLVD
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                                                                                                                                         STANDARD;
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5-ONE (BY SIMILARITY).
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                                                                                                                                         PRT;
                                                                                                                                         713 AA
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.ish-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Digitalis lanata (Foxglove).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae, euasterids I, Lamiales, Veronicaceae; Digitalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00221; PAL; 1.
TIGHTAMS, TIGR01226, phc_am_lyase, 1.
PROSITE, PS00488; PAL_HISTIDASE, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AJ002221; CAA05251.1; -. HSSP; P21310; 1B8F.
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                    418 MFAQFSELVNDFYNNGLPSNLSGGRNPSLDYGFKGGEIAMASYCSELQFLANPVTNHVQS
                                                                                                                                                                                                                                                      239
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                                                                                                                                                                                                                                                                                                                                   179
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                                                          360 QIEVIRTATKMIEREINSVNDNPLIDVSRNKALHCGNFQGTPIGVSMDNSRLAIASIGKL
                                                                                                358 QIEVIRSSTKMIEREINSVNDNPLIDVSRNKALHGGNFQGTPIGVSMDNTRLAIAAIGKL
                                                                                                                                                                                                               Z40 NSGLFFELQPKEGLALVNGTAVGSGLASIALYEANILSLLAEVMSAVFAEVMNGKPEFTD
                                                                                                                                                                                                                                                                                                                                                                       120 QGGALQKELIRFLNAGIFGNGTESTHTLPHSATRAAMLVRINTLLQGYSGIRFEILETIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 SQVAA1AAKDNE--VAVQLAESSKAGVKASSDWVMESMNKGTDSYGVTTGEGATSHRRTK 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59 SQVAGIAAANUSDTVKVELSEAARAGVKASSDWVMESMNKGTDSYGVTTGFGATSHPRTK 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 VENGHHGN---NGFCVKQNDPLNWVAAAEELKGSHLDEVKRMVEEFRKTVVKLGGETLTI 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MENGNHVNGVVNELCIK--DPLNWGVAAEALTGSHLDEVKKMVAEFRKPVVKLGGETLTV 58
                                                                                                                                                       HITHKLKHHPGQIEAAAIMEYILDGSDYVKAAQKVHEMDPLQKPKQDKYALKTSPQWIGP
                                                                                                                                                                                                                                                                                                                                                                                                           QGGALQKELIRFLNAGIFGNGTETSHTLPHSATRAAMIVRINTLLQGYSGIRFEILEAIT 178
                                                                                                                                     HLTHKLKHHPGQIEAAAIMEHILDGSSYVKAAQKMHEMDPLQKPKQDRYALRTSPQWLGP
                                                                                                                                                                                                                                                    EGG-FFELQPKEGLALVNGTAVGSGMASMVLFDANVLALLSEVLSAIFAEVMQGKPEFTD
                                                                                                                                                                                                                                                                                            KFLNHNITPCLPLRGTITASGDLVPLSYIAGLLTGRPNSKAVGPNGESLNAEQAFKLAGA
                                                                                                                                                                                                                                                                                                                                 KFLNNNITPCLPLRGTITASGDLVPLSYIAGLLTGRPNSKAVGPTGEVLNAEKAFAAAGV
Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  713 AA; 77732 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85.0%; Score 3096;
84.0%; Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MODIFIED TO FORM 4-METHYLLDENE-IMIDAZOLE: 5-ONE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  747CE64C65BDCC6A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         No. le-184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 713;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56;
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                                                          419
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Pred. No. 3.2e-184;

K

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RESULT 14
PALL, STYHU
ID PALL, STYHU
DAC P4572
DT 01-NC
DT 01-NC
DT 15-JI
OC SPCT
OC CUT
CC SPCT
RT 15-JI
RA MAT
R
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Highinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBH outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Manners J.M., McIntyre C.L., Nourse J.P.;
"Cloning and sequence of a cDNA encoding phenylalanine anumonia-lyase from the tropical forage legume Stylosanthes humilis.";
plant Physiol. 108-1301-3302 (1995).
-i- FUNCTION: THIS IS A KEY ENZYME OF PLANT METABOLISM CATALYZING THE FIRST REACTION IN THE HIOSYNTHESIS FROM L-PHENYLALANINE OF A WIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids 1; Fabales, Fabaceau: Panilionnidum. Accident
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-cv. Paterson; TISSUE-Stem; MEDLINE-95357421; PubMed-7630950;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STYHU
                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stylosanthes humilis (Townsville stylo).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Phenylalanine ammonia-lyase (EC 4.3.1.5).
                                                                                                                                                                                                                                  TIGREAMS; TIGRO1226, phe_am_lyase, 1. PROSITE; PS00488; PAL_HISTIDASE; 1.
                                                                                                                                                                                                                                                                                                                              Pfam; PF00221; PAL,
                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; L36822; AAA995@0,1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID-35628
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                                                                                                                                                                                                                                                                                                                                                                    InterPro
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                                                                                                                                                                                        yase; Phenylpropanoid metabolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 600 KNGENEKNASTSIFQKIEAFEAELKAVLPKEVESARVALEDGKPAIANRITECRSYPLYK 659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              420 MEAQESELVNDEYNNGLESNI.SGGRNESLDYGEKGSETAMASYCSELQELANEVTNHVQS 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PTM: CONTAINS AN ACTIVE SITE 4-METHYLIDENE-IMIDAZOLE-5-ONE (MIO) WHICH IS FORMED AUTOCATALYTICALLY BY CYCLIZATION AND DEHYDRATION OF RESIDUES ALA-SER-GLY (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VARIETY OF NATURAL PRODUCTS BASED ON THE PHENYLPROPANE SKELETON.

CATALYTIC ACTIVITY: L-phenylalanine - trans-cinnamate + NH(3).

PATHWAY: Phenylpropanoid biosynthesis; first step.

SUHCELLHIAR LOCATION: Cytoplasmic (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: BELONGS TO THE PAL / HISTIDASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NNGETEKNTNTSIFOKIATFEEELKVLLPKEVEGYRIAYENDTLSIPNPIKACRSYPLYR 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VAKRTLTTGVNGELHPSRFCELDLLRVVDREYVFAYVDDPCSATYPLMQKLRQVLVEHAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VAKKVLTMGVNGELHPSRFCEKDILLRVVDREYVFAYIDDVCSGTYPLMOKLRQVLVDHAL 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AEQHNQDVNSLGLISARKTAEAVDILKLMSSTYLVALCQSIDLRHLEENMKSTVKNTVSQ 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FIREELGTNFLTGEKVMSPGEECDRVFTAMSKGLIVDPLLKCLEGWNGAPLPIC 713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AEQHIQDVNSLGLISSRKTVEALDILKLMSSTYLVALCQAIDLKHLEENLRLSVKNTISQ 539
                                                                                                                                                                                                                                                                                                                                                                                                     P21310; 1B8F
                                                                                                                                                                                                                                                                                                                                                                IPRO01106: Phe/His_NH31yase.
                                                                               715 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                               77953 MW;
84.78;
Score 3088;
                                                                                                                     5-0NE
                                                                                                                                                  MODIFIED TO FORM 4-METHYLIDENE-IMIDAZOLE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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                                                                               ONE (BY SIMILARITY),
8D81EC3D5E4F6A2D CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (See http://www.isb-sib ch/announce/
D3 1;
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Length 715
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REPRESENTATION OF THE PROPERTY                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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049835;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Pel. 37, Last sequence update)
15-JUN-2002 (Pel. 41, Last annotation updat
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                                                                                                                                                                                                                                                                                                                             Lithospermum erythrorhizon.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Epermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Boraqinaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUN-2002 (Rel. 41, Last annotation update)
Phenylalanine ammonia-lyase 1 (EC 4.3.1.5) (PAL-1).
Biosci, Biotechnol, Biochem, 61:1995-2003(1997)
                            "CDNA cloning and gene expression of phenylalanine ammonia-lyase Lithospermum erythrorhizon.";
                                                                                                                                            SEQUENCE FROM N.A. MEDILINE-98101967; PubMed-9438980;
                                                                                                           Yazaki K., Kataoka M., Honda G., Severin K., Heide
                                                                                                                                                                                                                                                                    NCB1_Tax1D=34254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PALI_LITER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                678 EEFDRVFTAMCKGQJIDPLLECLGGWNGEPLPIC 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           622 EEELKTLLPKEVEGARIAYENGQSAIPNKIKECRSYPLYKFVREELGTEMLTGEKVRSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          618 EEELKVLLPKEVEGVRIAYENDTLSIPNRIKACRSYPLYRFVREELGRGFLTGEKVTSPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           498 EAVDILKLMSSTYLVALCQSIDLRHLEENMKSTVKNTVSQVAKKVLTMGVNGELHPSRFC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     442 LSASRNESLDYGEKGTETAMASYCSELQYLANEVTSHVQSAEQHNQDVNSLGLTSARKTN 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              382 DNPLIDVSRNKALHGGNFQGTPIGVSMDNTRLAVASIGKLMFAQFSELVNDFYNNGLPSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        378 UNPLIDVSPNKALHGGNEGGTFTGVSMDNTFLATAATGKLMFAQESELVNDFYNNGLPSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   322 HILDGSSYVKAAKKLHEIDPLQKPKQDRYALRTSPQWLGPLVEVIRFSTKSIEREINSVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 318 YILDGSDYVKAAQKVHEMDPLQKPKQDRYALRTSPQWLGPQTEVIRSSTKMTEREINSVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       198
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Matches 594; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TIGRRAMS; TIGR01226; phc_am_lyase; 1.
PROSITE; PS00488; PAL_HISTIDASE; 1.
Lyase; Phenylpropanoid metabolism; Multigene family
Lyase; Phenylpropanoid metabolism; Multigene family
SITE 196 198 MODIFIED TO FORM 4-MET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; D83075; BAA24928.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                           541 KVLTMGVNGELHPSRFCEKDLLRVVDREYVFAYIDDVCSGTYPLMQKLRQVLVDHALNNG
                                                                                                                                   480 HNQDVNSLGLISSRKTSEAVEILKLMSSSFLVALFQAVDLRHIEENVRLAVKNTVSQVAK 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      360 VIRSATKMIEREINSVNDNPLIDVSRNKALHGGNFQGTPIGVAMDNTRLAIASIGKLLFA 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     361 VIRSSTKMIEREINSVNUNPLIDVSRNKALHGGNFQGTPIGVSMUNTRLAIAAIGKLMFA 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         240 GFFELQPKEGLALVNGTAVGSGMASMVLYEANILAVLSEVISAIFAEVMNGKPEFTDHLT 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 LNNNITPCLPLRGTITASGDLVPLSYIAGLLTGRPNSKAVGPTGEVLNAEKAFAAAGVEG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 GALQKELIRFLNAGIFGNGTETSHTLPHSATRAAMIVRINTLLQGYSGIRFEILEAITKF 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 VAGIAAANDSDTVKVELSEAARAGVKASSDWVMESMNKGTDSYGVTTGFGATSHRRTKQG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MENGNHVNGVVNELCIKDPLNWGVAAEALTGSHLDEVKKMVAEFRKPVVKLGGETLTVSQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VAPIETY OF NATURAL PRODUCTS BASED ON THE PHENYLPPOPANE SKELETON CATALYTIC ACTIVITY: L-phenylalanine = trans-cinnamate + NH(3). PATHWAY: Phenylpropanoid biosynthesis; first step. SUBCHILDULAR LOCATION: Cytoplasmic (Probable). TISSUE SPECIFICITY: EXPRESSED MAINLY IN ROOTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OF RESIDUES ALA-SEK-GLY (BY SIMILARITY).
SIMILARITY: BELONGS TO THE PAL / HISTIDASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: THIS IS A KEY ENZYME OF PLANT METABOLISM CATALYZING THE FIRST REACTION IN THE BIOSYNTHESIS FROM L-PHENYLALANINE OF A WIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTM: CONTAINS AN ACTIVE SITE 4 METHYLIDENE-IMIDAZOLE-5 ONE (MIO). WHICH IS FORMED AUTOCATALYTICALLY BY CYCLIZATION AND DEHYDRATION
                                                                                                                                                                                                                                                                                                                                                    QFSELVNDFYNNGLPSNLSGGRNPSLDYGFKGGEIAMASYCSELQFLANPVTNHVQSAEQ 480
                                                                                                                                                                                                                      HNQDVNSLGLISARKTAEAVDILKLMSSTYLVALCQSIDLRHLEENMKSTVKNTVSQVAK 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HKLKHHPGQIEAAAIMEHILDGSGYVKAAQKLHEMDPLQKPKQUKYALRTSPQWLGPQIE 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HKLKHHPGQIEAAAIMEYILDGSDYVKAAQKVHEMDPLQKPKQDRYALRTSPQWLGPQIE 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GFFELQPKEGLALVNGTAVGSGMASMVLFDANVLALLSEVLSAIFAEVMQGKPEFTDHLT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LNTNITPCLPLRGTITASGDLVPLSYIAGLLTGRPNSKAVGPTGEKINAEEAFRLAGIST 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GALQKELIRFLNAGIFGNGTETSHTLPHSATRAAMLVRINTLLQGYSGIRFEILEAITKF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VENG----NGKTMEFCMKDPLNWEMASESMKGSHLDEVKNMVAEFRKPVVQLAGKTLTIGQ 61
                                                                                                                                                                                                                                                                                                    QFSELVNDYYNNGLPSNLTGSRNPSLDYGFKGAELAMASYCSELQFLANPYTNHVQSAEQ 479
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IPR001106; Phe/His_NH3lyase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84.5%; score 3077.5; DB 1; Length 710; 83.5%; Pred. No. 1.4e-183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59; Indels
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Search completed: March 29, 2003, 02:10:56 Job time: 42 secs

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Minimum DB seq length: 0
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    BLOSUM62
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3644
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Listing first 45 summaries
                                                                                                                                                                                                                        SPTREMBL_21:*
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Copyright (c) 1993 - 2003 Compugen Ltd.
sp_unclassified:*
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2325.389 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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619	655	687	717	725	715	718	712	716	710	711	721	708	730	716	711	Length
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Q39545	Q9XGR3	Q941'90	Q8RWP4	094AN1	024266	Q9XFX6	Q94F89	Q9ATN7	Q94C45	09AX15	Q9XFX5	Q94 EN0	Q9M567	Q9MAX1	Q8W2E4	SUMMARIES
Q39545 cucumis mel	Q9xgr3 vigna ungui	Q94f90 manihot esc		094anl arabidopsis			Q94f89 manihot esc	-		Q9axi5 pharbitis n	Q9xfx5 citrus clem	Q94en0 rehmannia q	Q9m567 rubus idaeu	Q9max1 catharanthu	Q8w2c4 lactuca sat	Description

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Q9M626	041293	082476	093967	Q9M627	Q940D8	Q9LEH2	Q9M3U1	09LEP1	080406	Q94F91	Q43211	Q8S3W3	Q9SDW2	810.46Ō	Q9FUI7	©a≅ <b>M</b> C8	Q8VWP6	004869	004875	UU4876	Q9FT38	Q8SAS6	Q8SAS7	QBRV49	Q8RUZ3	C81647	28 <b>VX</b> G7	Q9FS00
	Q41293 sorghum bic	082476 manihot esc	C)		Q940d8 brassica ra	©91ch2 juqlans niq			-		Q43211 triticum ae			_				004869 hordeum vul			tritic	e sunid		pinus sy	pinus sy	" capsicum	rea mays	ç91s00 dianthus ca

## ALIGNMENTS

RESULT OF REAL PROPERTY	8WZE4 PRELIMINARY; PRT; 711 AA.  8WZE4;  1-MAR-2002 ("TEMBLITC1: 20, Created)  1-MAR-2002 ("TEMBLITC1: 20, Last sequence update)  1-UN-2002 ("TEMBLITC1: 21, Last annotation update)  herylalanine ammonia-lyase, actuca sativa (Garden lettuce).  ukaryota, Viriaiplauldae, Strephophyta, Embryophyta; Tracheoph permatophyta; Magnoliophyta; eudicotyledons; core eudicots; steridae, euasterids il, Asterales, Asteraceae, Lactuceae; La CBI_TaxID-4236;  EQUENCE FROM N.A.  Characterization of phenylalanine ammonia-lyase (PAL) gene in ettuce leaf tissue.";  ubmitted (AUG-2000) to the EMBL/GenBank/DDHJ databases.
D R R R P P P P P P P P P P P P P P P P	SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE FROM N.A. Submpos-Vargas R., Nonogaki H., Suslow T., Saltveit M.; "Characterization of phenylalanine ammonia-lyase (PAL) gene in wounded lettuce leaf tissue." Submitted (AUG-2000) to the EMBL/GenHank/NNHJ databases. EMBL; AF299330; AAL55242.1;
다 다 다 다 다 다	EMBL; AF299330; AAL52242.1; InterPro; IPR001106; Phe/His_NH31yase. Plam; FF00221; PAL, 1.
SO	PROSITE; PS00488; PAL_HISTIDASE; UNKNOWN_1. Lyase. SEQUENCE 711 AA; 77363 MW; 3120AB2877C29513 CRC64;
M B Q	Query Match 100.0%; Score 3644; DB-10; Length 711; Bost Local Similarity 100.0%; Prod No. 9 76-233; Matches 711, Conservative 0, Mismatches 0; Indels 0; Gaps
Ph 49	1 MENGNHVNGVVNELCIKDPLNWGVAAEALTGSHLDEVKKMVAEFRKPVVKLGGETLTVSO 60 
γ ₀	61 VAGIAAANDSDYVKVELSEAARAGVKASSGWVMESMNKGTDSVGVTTGFGATAGAFSTAGFTGLIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII

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                               Matches 617;
                                                                                                                                                                                                                                                                                                         Catharanthus roseus (Rosy periwinkie) (Madagascar periwinkie). Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; endicotyledons; core endicots; Asteridae; euasterids I; Gentianales; Apocynaceae; Rauvolfioideae; Asteridae; euasterids I; Gentianales; Apocynaceae; Rauvolfioideae;
                                                                                                                                                                                           "cDNA of phenylalanine ammmonia lyase from Catharanthus roseus."; Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AB042520; BAA95629.1; -.
                                                                                                                                                                                                                                                                                                                                                                            O9MAX1;

01-0CT-2000 (TrEMBLrel. 15, Created)

01-0CT-2000 (TrEMBLrel. 15, Last sequence update)

01-JUN-2002 (TrEMBLrel. 11, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                      Phenylalanine ammonia lyase
                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9MAX1
                                                                                        SEQUENCE
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                                                                                                                    PROSITE;
                                                                                                                                   TIGRFAMS,
                                                                                                                                                                               HSSP;
                                                                                                                                                                                                                                       Kiyota S.,
                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                NCBI_TaxID=4058;
                                                                                                                                                                 InterPro;
                                                                                                       yase
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                                            Local Similarity
2 ENGNHVNGVVNELCIKDPLNWGVAAEALTGSHLDEVKKMVAEFRKPVVKLGGETLTVSQV
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                                                                                                                                                                             P21310;
                                                                                                                                                PF00221; PAL; 1
                                                                                                                  PS00488; PAL_HISTIDASE;
                                                                                                                                   TIGR01226; phe_am_lyase, 1.
                                                                                                                                                               IPR001106; Phe/His_NH3lyase
                                                                                        716 AA;
                                                                                                                                                                                                                                       Sakano K., Kim J.;
                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                               188F
                                                                                        78241 MW; 1F16D4DEB8683B0B CRC64;
                                        87.7%; Score 3195 5; DR 10; Length 716; 86.9%; Pred No. 2.8e-194;
                             43; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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expression, and evolution.";
Plant physiol. 127:230-239(2001).
EMBL AF237955 AAF40224.1, -
HSSP; P21310; 188F.
                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae, Streptophyta; Embryophyta; Tracheo; Spermatophyta; Magnoliophyta; eudicotyledons, core eudicots, eurosids 1, Rosales; Rosaceae; Rosoideae, Rubus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 21, Last annotation update)
Phenylalanine ammonia-lyase 2 (EC 4.3.1.5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9M567;
Pfam; PF00221; PAL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rubus idaeus (Raspberry).
                                                                                                                                                                                                                                    Kumar A., Ellis B.E.
                                                                                                                                                                                                                                                                   MEDLINE=21437948;
                                                                                                                                                                                                                                                                                                                                                                    NCBI\_TaxID=32247;
                               InterPro; IPR001106; Phe/His_NH31yase
                                                                                                                                                                                              "The phenylalanine ammonia-lyase gene family in raspberry. structure
                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               547 TLTVGVNGELHPSRFCEKDLIRVVDREYVFAYVDDPCSGTYPLMEKLRQVIVDHALQNGE
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                                                                                                                                                                                                                                                                   PubMed=11553751;
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RESULT 4
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                                         Phenylalanine ammonia-lyase (EC 4.3.1.5).
                                                                             01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                              Q94EN0;
                                                                                                                                                                    094 EN0
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                     Rehmannia glutinosa
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                                                                                                                                                                                                                                                                     724 GEPLPIC 730
                                                                                                                                                                                                                                                                                                            705 GEPLPIC 711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     165 GYSGIRFELLEAITKELNNNITPCLPURGTITASGDLVPLSYIAGLLTGRPNSKAVGPTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66 REPVELIGETITISQUAAL--ANHDSGUKVELAESARAGUKASSDWVMDSMNKGTDSYG 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNTRLAIAAIGKLMFAQFSELVNDFYNNGLPSNLSGGRNPSLDYGFKGGEIAMASYCSEL 464
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                                                                                                                                                                                                                                                                                                                                                                           NRIKACRSYPLYRFYREELGRGFLTGEKYTSPGEEFDRYFTAMCKGQIIDPLLECLGGWN 704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QFLANPYTNHVQSAEQHNQDVNSLGLISARKTAEAVDILKLMSSTYLVALCQSIDLRHLE 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNTRLATASIGKLMFAQFSFLVNDFYNNGLPSNLSGGRDPSLDYGFKGAETAMASYCSEL 483
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                                                                                                                                                                                                                                                                                                                                                                                                                                   MORLROVLVEHALTINGENEKNASTSIFOKITAFEEELKTILPKEVESARAAYESGNAAIP 663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENLKSTYKNTYSQLAKRYLTTGYNGELHPSRFCEKDLLMYVEREYLFAYIDDPCSATYPL 603
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MQKLRQVLVDHALNNGETEKNTNTSIFQKIATFEEELKVLLPKEVEGVRIAYENDTLSIP 644
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                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86.4%; Score 3148.5;
83.9%; Pred. No. 2.8;
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Best Local .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rhemannia glutinosa."; Submitted (JUL-2001) to the EMBL/GenHank/DDHJ databases EMHL, AF401636; AAKB4225.1; -
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PKOSITE; PS00488; PAI_HISTIDASE; UNKNOWN_1.
PKOSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yun S.J., Lee B.K., Park M.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Spermatophyta, Magnoliophyta; endicotyledons; core endicots;
Asteridae; enasterids I; Lamiales; Lamiales incertae sedis; Rehmannia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro:
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                                                                                                                                                                                                                                                     475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Molecular characterization of phenylalanine ammonia lyase
655
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                                                                                                                           598
                                                                                                                                                                                                                                                                                                                                                                                                                              355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              236 V-SGFFELQPKEGLALVNGTAVGSGLASIALYDANILAVLSEVTSVIFAEVMNGKPEFTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             295 HUTHKLKHHPGQIEAAAIMEHILDGSAYVKAAQKLHETDPLØKPKQDRYALRTSPQWLGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              y Match 85.3%; Score 3107.5; DB 10; Length 708;
Local Similarity 84.3%; Pred. No. 1.1e-188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MENGNHVNGVVNELCI---KDPLNWGVAAEALTGSHLDEVKKMVAEFRKPVVKLGGETLT
                    FVREELGRGFLIGEKVISPGEEFDRVFIAMCKOQIIDPLLECLGGWNGEPLPIC 711
                                                                                                                                                                                                                                                                                                                                                             MFAQFSELVNDFYNNGLPSNLSGGRNPSLDYGFKGGELAMASYCSELQFLANPVINHVQS
                                                                                                                                                                                                        VAKKVLTMGVNGELHPSRECEKDLLRVVDREYVFAYIDDVCSGTYPLMQKLRQVLVDHAL
                                                                                                                                                                                                                                                                                                                                                                                                                            QIEVIRTATKMIEREINSVNDTPLIDVSRNKALHGGNFQGTPIGVSMDNTKLAIAAIGKI. 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QIEVIPSSTKMTEREINSVNDNPLIDVSRNKALHGGNEQGTRIGVSMDNTRLAIAAIGKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VEGGFFELQPKEGLALVNGTAVGSGMASMVLFDANVLALLSEVLSATFAHVMQGKPEFTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KQGGALQKELLRELNAGTEGNGTETSHTLPHSATRAAMTVRINTLLQGYSGTREETLEAT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MENGHHHS---NGLCVETTRÜPLNWVAAAESLKGSHLDEVKRMVEEERKPAVKLGGESLT 57
FIREELGTNYLTGEKVVSPGEECDKVFTALSKGLIVDPLLKCLEGWNGAPPPIC 708
                                                                            NNGESEKNVSTSIFOKIEAFEVELKAILPKEVESARIALESGNPAIGNRITECRSYPLYK
                                                                                                                       NNGETEKNITNISTE OKTATE EBELKVILLEKEVEGVETAYENDILLSTENETKACKSYPLYK
                                                                                                                                                                  VAKRTLITMG1NGELHPSRFCEKDLLRVVDREYVFAY1DDPCSGTYPLMQKLRQVLVDHAL
                                                                                                                                                                                                                                                   AEQHNQDVNSLGLISSRKTVEALDILKLMSSTYLIALCQAVDLRHLEENLRLSVKNTVSQ
                                                                                                                                                                                                                                                                                           AEQHNQDVNSLGLISARKTAFAVDILKLMSSTYLVALCQSIDLRHLEENMKSTVKNTVSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HITHKIKHHPGQIEAAAIMEYTIDGSDYVKAAOKVHEMDPLQKPKQDRYALKISPOWLGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TKFLNHNITPCLPLRGT1TASGDLVPLSY1AGLLTGRPNSKAVGPNGEALNAGEAFSLAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VSQVAGIAAANDSDTVKVELSEAARAGVKASSDWVMESMNKGTDSYGVTTGFGATSHRRT 117
                                                                                                                                                                                                                                                                                                                                      MFÄQFSELVNDFYNNGLESNLSGGRNESLDYGFKGSEIAMASYCSELQFLANEVTNHVQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KQGGALQKELIRFLNAGIFGNGTESNHALPHSATRAAMLVRINTLLQGYSGIRFEILEAL 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 602;
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RESULT 5
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09xFX5;
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
phenylalanine-ammonia lyase (EC 4.3 1 5)
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EMBL: AJ238753; CAB42793.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIGRFAMs;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sanchez-Ballesta M.T., Lafuente M.T., Zacarias L., Granell A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-CV.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 234 AAAGVEGGFFELQPKEGLALVNGTAVGSGMASMVLFDANVLALLSEVLSAIFAEVMQGKP 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 114 HRRTKQGGALQKELIRFLNAGIFGNGTETSHTLPHSATRAAMIVRINTLLQGYSGIRFEI 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MENGNHVNGVVNELC-----IKDPLNWGVAAEALTGSHLDEVKKMVAEFRKPVVKLGGE 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WLGPQIEVIRSSTKMIEREINSVNDNPLIDVSRNKALHGGNFQGTPIGVSMDNTRLAIAA 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TLTVSQVAGIAAANDSDT-VKVELSEAARAGVKASSDWVMESMNKGTDSYGVTTGFGATS 113
TVSQVARKVLTVGANGELHPSRFCEKDLLKAADREHVFAYIDDPCSATYPLMQKLRQVLV
                                                                                                                                                                                                                             HVQSAEQHNQDVNSLGLISARKTAEAVDILKLMSSTYLVALCQSIDLRHLEENMKSTVKN 533
                                                                                                                                                                                                                                                                                                                                                                                 IGKLMFAQFSELVNDFYNNGLPSNLSGGRNPSLDYGFKGGELAMASYCSELQFLANPVTN 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                       WLGPQIEVIRFATKSIEREINSVNDNPLIDVSRNKALHGGNFQGTPIGVSMDNTRLAIAA 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KQAGE - - GEFELQPKEGLALVNGTAVGSGLASMYLFDANNLALLSEILSAIFAEVMQGKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LEAITKFLNNNITPCLPLRGTITASGDLVPLSYIAGLLTGRPNSKAVGPTGEVLNAEKAF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TLTVAQVAATATAGDVNAQVKVELSESAPEGVKASSDWVMDSMNKGTDSYGVTTGFGATS
                                                                                                                                                       HVQSAEQHNQDVNSLGLISSKKTAEAVDILKLMSSTFLVALCQAIDLRHLEENLKHTVKD
                                                                                                                                                                                                                                                                                                       LGKLMFAQFSELVNDFYNNGLPSNLSGGRNPSLDYGFKGAETAMASYCSELQFLANPVTN 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EFTDHLTHKLKHHPGQIEAAAIMEHILDGSSYVKAAKKLHEIDPLQKPKQDRYALRTSPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EFTDHLTHKLKHHPGQIEAAAIMEYILDGSDYVKAAQKVHEMDPLQKPKQDRYALRTSPQ 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LDAITKELNHSITPCLPLRGTITASGDLVPLSYIAGLLTGEPNSKATGPNGEIIDAQEAS
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AMs; TIGR01226; phe_am_lyase; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FORTUNE: TISSUE=FLAVEDO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85.2%; Score 3106; DB 10; 84.3%; Pred. No. 1.4e-188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48; Mismatches 55;
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Q9AXI5;
Q1-JUN-2001 (TrEMBLrel. 17, Created)
Q1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Phenylalanine ammonia-lyase (EC 4.3.1.5).
Pharbitis nil (Violet) (Japanese morning qlory).
Pharbitis nil (Violet) (Japanese morning clory).
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TIGRFAMS; TIGR01226; phe_am_lyase; 1.
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420 AQFSELVNDYYNNGLPSNLTAGRNPSLDYGFKGAEIAMASYCSELQFLANPVTNHVQSAE
                                                                              420 AQFSELVNDFYNNGLPSNLSGGRNPSLDYGFKGGETAMASYCSELQFLANPVTNHVQSAE 479
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                                                                                                                                                                                                                                                                                                              300 THKLKHHPGQIEAAAIMEHILDGSSYVKAAQKMHEMDPLQKPKQDRYALRTSPOWLGPQI 359
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                                                                                                                                                         360 EVIRAATKMIEREINSVNDNPLIDVARSKALHGGNFQGTPIGVSMDNSRLALASIGKILF 419
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Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL: AY036011, AAK62030.1.
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta: Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
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01-DEC-2001 (TERMBLEEL 19, Last sequence ipdate)
01-JHW-2002 (TERMBLEEL 21, Last annotation update)
Phenylalanine ammonia-lyase 1 (EC 4.3.1.5).
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TIGRFAMs; TIGR01226; phe_am_lyase;
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                                     *** TIDOSDYYKAAQKYHEMDPLQKPKQDRYALRTSPQWLGPQTEVTRSSTKMTERETNSVN 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NGTETSHTLPHSATRAAMIVRINTLLQGYSGIREEILEAITKFLNNNITPCLPLRGTITA 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEAARAGVKASSDWVMESMNKGTDSYGVTTGFGATSHKKTK@$GALQKELIFFLNAGIFG 137
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HVLDGSSYIKAAQKVHEIDPLQKPKQDRYALRTSPQWLGPQIEVIRTATKMIEREINSVN
                                                                                                                                                                                                                                                                             SGDLVPLSY1AGLLTGRPNSKSLGPNGESLDAARAFKLAGINGGFFELQPKEGLALVNGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SHEARAGVKASSDWVLDSMNKGTDSYGVTTGFGATSHRRTKQGGALQRELIRFLNAGIFG 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DPLNWGMAAESLKGSHIDEVKRWVDEYRKPVVRLGGETLTIAQVTAI--ANHDSGVKVEL 76
                                                                                                                                    AVGSGLASMVLFEANVLAVLSEVLSALFAEVMLGKPEFTDHLTHKLKHHPGQLEAAALME
                                                                                                                                                                                                            AVGSGMASMVLEDANVLALLSEVLSAIFAEVMOGKPEFTDHLTHKLKHHPGQIEAAAIME 317
                                                                                                                                                                                                                                                                                                                                                     SGDLVPLSY LAGLLTGRPNSKAVGPTGEVLNAFKAFAAAGVEGGFFELQPKEGLALVNGT 257
                                                                                                                                                                                                                                                                                                                                                                                                                             NGQESCHTLSHTATRAAMLVRINTLLQGYSGIRFEILEAITKFINNNVTPRLPLRGTITA 196
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85.3%; Pred. No. 9
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RESULT 8
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QSAIN;
01-JUN-2001 (TrEMBLrel 17, Created)
01-JUN-2001 (TrEMBLrel 17, Last seq
01-JUN-2002 (TrEMBLrel 21, Last ann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TICRPAMS; TICR01226; phc_am_lyase; PROSITE; PS00488; PAL_HISTIDASE; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kim J.-B.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kim J.-B., Kim J.-B., Cho K.-J., Woon U., Ha S.-H., Molecular Cloning and Characterization of Phenylal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        497
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177 ITKELNNNITPOLPLROTITASGDLYPLSYIAGLLIGEPNSKAVGPIGEVLNAEKAFAAA
                                                                                                                                                                                                                              64 TISQVAAIAAKUNA--VAVELAESAFAGVKASSDWVMDSMSKGIDSYGVIIGIGATSHER 121
                                                                                                                                                                                                                                                                                                                                                                              4 NGHHOSNGHNNOANGFOVKONDULNWAAAAFSI.KGSHI.FFVKKWVFFFFVKFVVKI.GGETI. 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 NGNH----VNGVVNELCIK--DPLNWGVAAEALTGSHLDEVKKMVAEFPKPVVKLGGETL 56
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                                                                                                                                                   TKQGGALQKELLRELNAGIEGNGTETSHTLPHSATRAAMIVRINTLLQGYSGIREEILEA
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Phenylalanine ammonia-lyase 2 (EC 4.3.1.5).
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                                                                                                                                                                                                                                                                              Pfam; PF00221; PAL; 1.
TIGRFAMS; TIGR01226; phe_am_lyase,
                                                                                                                                                                                                                                                                                                                                        Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases EMBL; AF383152; AAK60275.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q94F89
                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                           PROSITE; PS00488; PAL_HISTIDASE; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=3983;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Manihot esculenta (Cassava) (Manioc)
                                                                                                                                                                                                                                          Lyase
                                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                                               "Phenylalanine ammonia-lyase 2 gene, PAL2,
                                                                                                                                                                                                                                                                                                                                                                                                  Li H., Beeching J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            182 ITKFLNQNVTPCLPLPGTITASGDLVPLSYIAGLLTGRPNSKAVGPAGEPLTAEQAFKLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    242 GVTGGFFDLQPKEGLALVNGTAVGSGLASIALFDANVLAVLSVVMSPVFAEVMNGKPEFT
                    61
                                                            6
                                                                                                                                                           Local Similarity
                  VAGIAAANDSDTVKVELSEAARAGVKASSDWVMESMNKGTDSYGVTTGFGATSHPPTKQG 120
                                                        QNG-HQNGSLDSLCTARDPLNWGLAAESMSGSHLDEVKKMVAEFRKPLVKLGGETLTVAQ 64
                                                                                               ENGNHVNGVVNELC-IKDPLNWGVAAEALTGSHLDEVKKMVAEFRKPVVKLGGETLTVSQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KFIREELGTGFLTGEKAVSPGEECEKVFAALSNGLTIDPLLECLQGWNGEPLPTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REVREELGRGFLTGEKVTSPGEEFDRVFTAMCKGQIIDPLLECLGGWNGEPLPIC 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LKNGESEKNVSTSIFHKIEAFEEELKALLPKEVESARIALESGSPAVANRIEECRSFPLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LNNGETEKNTNTSIFQKIATFEEELKVLLPKEVEGVRIAYENDTLSIPNRIKACRSYPLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SAEQHNQDVNSLGLISSRKTVEALDILKLMSSTYLVALCQAVDLRHVEENMKLAVKNTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LLFAQFSELVNDFYNNGLPSNLSGGRNPSLDYGFKGSEIAMASYCSELQFLVNPVTNHVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PQIEVIRSSTKMIEREINSVNDNPLIDVSKNKALHGGNPQGTPIGVSMDNTRLAIAAIGK 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DHITHKLKHHPGQTEAAAIMEHILUGSGYYKAAQKLHEIDPLQKPKQDKYALKTSPQWLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DHLTHKLKHHPGQI BAAAIMEYILDGSDYVKAAQKVHEMDPLQKPKQDRYALRTSPQWLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QVAKRTLTMGVNGELHPSRFCEKELIRVVDREYVFTYIDDPCLATYPLMQKLRQVLVDHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QVAKKVLTMGVNGELHPSRFCEKDLLRVVDREYVFAYIDDVCSGTYPLMQKLRQVLVDHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SAEQHNQDVNSLGLISARKTAEAVDILKLMSSTYLVALCQSIDLRHLEENMKSTVKNTVS 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LMFAQFSELVNDFYNNGLPSNLSGGRNPSLDYGFKGGETAMASYCSELQFLANPVTNHVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PQIEVIRTATKMIEREINSVNDNPLIDVSRNKAIHGGNFQGTPIGVSMDNTRLAIASIGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GVEGGFFELQPKEGLALVNGTAVGSGMASMVLFDANVLALLSEVLSATFAEVMQGKPEFT
                                                                                                                                                                                                                                                                                                                   IPR001106; Phe/His_NH3lyase
                                                                                                                                                                                                                        712 AA;
                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
84.6%; Score 3084.5; DB 1 83.4%; Pred. No. 3.1e-187;
                                                                                                                                                                                                                        77462 MW;
                                                                                                                                       62; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                      99F14CB9D0DEA34D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          712 AA
                                                                                                                                                                                                                                                                                                                                                                             from cassava.";
                                                                                                                                                                          DB 10, Length 712,
                                                                                                                                         Indels
                                                                                                                                       ٥,
                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                   "Phenylalanine ammonia-lyase gene expression in response to temperature in mandarin fruit."; Submitted (MAY 1999) to the EMBL/GenBank/DDBJ databases. EMBL; AJ238754; CAB42794.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         eurosids II; Sapindales; Rutaceae; Citrus. NCHI_TaxID=93374;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Citrus clementina x Citrus reticulata.
Eukaryota; Viridiplantae, Streptophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9XFX6;
SEQUENCE
                                                                    PROSITE; PS00488; PAI_HISTIDASE;
                                                                                               Pfam; PF00221; PAL; 1.
TIGRFAMs; TIGR01226; phe_am_lyase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Spermatophyta, Magnollophyta, eudicotyledons; core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                            Sanchez-Ballesta M.T., Lafuente M.T., Zacarias L., Granell A.
                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=CV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Phenylalanine-ammonia lyase (EC 4.3.1.5).
                                                                                                                                                                                                                     HSSP; P21310; 1B8F
                                                                                                                                                                                  nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                662 EEIGTGLLTGEKIRSPGEEFDKVFTAMCQGKILDPMLDCLKEWNGAPLPIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     661 EELGKGFLIGEKVTSPGEEFUKVFTAMCKGQIIDPLLECLGGWNGEPLPIC 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          541 KVLTMGVNGELHPSRFCEKDLLRVVDREYVFAYIDDVCSGTYPLMQKLRQVLVDHALNNG
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                                                                                                                                                                               IPR001106; Phe/His_NH3lyase
                                                                                                                                                                                                                                                                                                                                                                                                                                      FORTUNE; TISSUE=FLAVEDO;
718 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
78037 MW; 4C08C8F3232B3EF6 CRC64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 718 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Embryophyta; Tracheophyta,
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Phenylalanine ammonia-lyase (EC 4.3.1.5).
                           Osakabe Y., Ohisubo Y., Kawai S., Katayama Y., Moroboshi N.:
"Structures and tissue-specific expression of genes for phenylalanine ammonia-lyase from a hybrid aspen, Populus kitakamiensis.",
Plant Sci. 105.217.226(1995).
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Pfam; PF00221; PAL; 1.
PRINTS; PR01568; LYMPHOTACTNP
TIGREAMs: TIGR01226; phe_am_lyase; 1.
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                                           648 KACRSYPLYRFVREEIGRGFLTGEKVTSPGEEFDRVFTAMCKGQIIDPLLECLGGWNGEP 707
                                                                                                                                                                                            542 RQTVKNTVSQVAKKVLTTGVNGELHPSRFCEKDLLKVVDREQVYTYADDPCSATYPLIQK 601
                                                                                                                                                                                                                                                                                                                 468 ANPVTNHVQSAEQHNQDVNSLGLISARKTAEAVDILKLMSSTYLVALCQSIDLRHLEENM
                                                                                                                                                                                                                                                                                                                                                                                           422 RLAIAAIGKLMFAQFSELVNDFYNNGLPSNLTASRNPSLDYGFKGAEIAMASYCSELQYL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         362 LRTSPQWLGPQIEVIRYATKSIEREINSVNDNPLIDVSRNKAIHGGNFQGTPIGVSMDNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       302 VMSGKPEFTDHLTHRLKHHPGQ1EAAAIMEHILDGSSYMKLAQKLHEMDPLQKPKQDRYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     288 VMQGKPEFTDHLTHKLKHHPGQIEAAAIMEYILDGSDYVKAAQKVHEMDPLQKPKQDRYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   242 TAEEAFKLAGISSGFFDLØPKEGLALVNGTAVGSGMASMVLFETNVLSVLAEILSAVFAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 228 NAEKAFAAAGVEGGFFELQPKEGLALVNGTAVGSGMASMVLFDANVLALLSEVLSALFAE 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                168 GIRFEILEAITKFLNNNITPCLPLRGTITASGDLVPLSYIAGLLTGRPNSKAVGPTGEVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 GFGATSHRRTKNGVALQKELIRFLNAGIFGSTKETSHTLPHSATRAAMLVRINTLLQGFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    182 GIRFEILEAITSFLNNNITPSLPLRGTITASGDLVPLSYIAGLLTGRPNSKATGPNGEAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             108 GFGATSHRRTKQGGALQKELIRFLNAGIFGNGTETSHTLPHSATRAAMIVKINTLLQGYS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 NGAHKSNGGGVDAMLCGGDIKTKNMVINAEDPLNWGAAAEQMKGSHLDEVKRMVAEFFKP 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 NGNHVN---GVVNELC-----IKDPLNWGVAAEALTGSHLDEVKKMVAEFRKP 47
KECKSYPLYRFYREELGTELLTGEKYTSPGEEFDKVFTAICEGKIIDPMMECLNEWNGAP
                                                                                                                                                                                                                                                                                          ANPVTSHVQSAEQHNQDVNSLGLISSRKTSEAVDILKLMSTTFLVAICQAVDLRHLEENL
                                                                                                                                              LRQVLVDHALNNGETEKNTNTSIFQKIATFEEELKVLLPKEVEGVRIAYENDTLSIPNRI
                                                                                                                                                                                                                                       KSTVKNTVSQVAKKVLTMGVNGELHPSRFCEKDLLRVVDREYVFAYIDDVCSGTYPLMQK
                                                                                              LRQVIVDHALINGESEKNAVTSIFHKIGAFEEELKAVLPKEVEAARAAYDNGTSAIPNRI
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81.4%; Pred. No. 9.6
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Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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490 DVNSLGLISSKRISEAVDIEKEMSTTFLVGICQAVDLKHLEENLKQTVKNIVSQVAKKVI. 549
                                                                              484 DVNSLGLISARKTAEAVDILKLMSSTYLVALCQSIDLRHLEENMKSTVKNTVSQVAKKVL
                                                                                                                                                                                                                                           424 ELVNDFYNNGLPSNLSGGRNPSLDYGFKGGEIAMASYCSELQFLANPYTNHVQSAEQHNQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       244 ELQPKEGLALVNGTAVGSGMASMVLFDANVLALLSEVLSAIFAEVMQGKPEFTDHLTHKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            130 QTELIRFLNAGIFGNTKETCHTLPQSATRAAMLVRVNTLLQGYSGIRFEILEAITSLLNH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124 QKELIRFLNAGIFGNGTETSHTLPHSATRAAMIVPINTLLQGYSGIPFEILEAITKFLNN 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IAAANDSDTVKVELSEAARAGVKASSDWVMESMNKGTDSYGVTTGFGATSHRRTKQGGAL 123
                                                                                                                                                                 ELVNDFYNNGL/PSNLTASSN/PSLDYGFKGAELAMASYCSELQYLAN/PVTSHVQSAEQHNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82.6%; Score 3009;
81.6%; Pred. No. 2
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RESULT 14
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01-DEC-2001 (TERMELTE: 19, Last sequence update)
01-JUN-2002 (TERMELTE: 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota: Viridiplantae, Streptophyta, Embryophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eneurosids I, Malpighiales, Euphorblaceae; Manihot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q94F90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Phenylalanine andonia-lyase 1 gene, PAL1, from cassava.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL: AF383151; AAK60274.1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Phenylalanine ammonia-lyase 1 (EC 4.3.1.5) (Fragment). PAL1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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Pfam; PF00221; PAL; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID-3983;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00488; PAL_HISTIDASE; UNKNOWN_1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A
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UNPLIDVSKNIALHGGNEGGTETGVSMUNTKLATASTGKLMTAGESELVNDEYNNGLESN 436
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                                                                           SGDLVPLSYTAGLLTGRPNSKAVGPTGEVLNAEKAFAAAGVEGGFFELQPKEGLALVNGT 257
                                                                                                                                                                                                                                                                                                                             NGTETSHTLPHSATRAAMIVRINTLLQGYSGIRFEILEAITKFLNNNITPCLPLRGTITA 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                             DPLNWGMAAESLKGSHIDEVKRMVDEYRKPVVRLGGEIL/TIAQVTAI -- ANHDSGVKVEL 76
                                       DNPLIDVSRNKALHGGNFQGTPIGVSMDNTRLAIAAIGKLMFAQFSELVNDFYNNGLPSN 437
                                                                                                                 YILDGSDYVKAAQKVHEMDPLQKPKQDRYALRTSPQWLGPQIEVIRSSTKMIEREINSVN 377
                                                                                                                                                       AVGSGLASMVLFEANVLAVLSEVLSATFAEVMLGKPEFTDHLTHKLKHHPGQTEANAIME
                                                                                                                                                                                             AVGSGMASMVLEDANVLALLSEVISATEAEVMQGKPEETDHLTHKIKHHPGQTEAAATME 317
                                                                                                                                                                                                                                 SCHLAPLSYTAGLITECPPNSKSLCPNGESLHAAEAFKLAGINGGFFELQPKEGLALVNGT 256
                                                                                                                                                                                                                                                                                                           NGQESCHTLSHTATRAAMLVRINTILLQGYSGIRFEILEAITKFINNNVTPRLPLRCTITA 196
                                                                                                                                                                                                                                                                                                                                                                                   SEEAPAGVKASSDWVLDSMNKGTDSYGVTTGFGATSHFFTK@GGALQKELIFFLNAGIFG
                                                                                                                                                                                                                                                                                                                                                                                                                       SEAARAGVKASSDWVMESMNKGTDSYGVTTGEGATSHRRTKQGGALQKELLRFLNAGIEG 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Beeching J.R.;
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75065 MW; 950A63AlA4BE3D76 CPC64;
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85.8%; Pred No 1 4e-181;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49; Mismatches
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01-NOV-1999 (TEMBLEE) 12,
01-NOV-1999 (TEMBLEE) 21,
01-JUN-2002 (TEMBLEE) 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Isolation of phenylalanine ammonia:lyase gene from Vigna unguiculata, challenged by cucumber mosaic virus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ū9XGR3
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                                                                                                                                                    180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        618 BEELKVILLPKEVEGVRIAYENDTLSIPNRIKACKSYPLYRFVREELGRGFLIGEKVISPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 116 KTKQGGALQKELIFFLNAGIFGNGTETSHTLPHSATPAAMIVPINTLLQGYSGIRFEILE 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56 LIVSQVAGIAAANUSUIVKVELSEAAKAGVKASSUWVMESMNKGIDSYGVITGEGATSHR 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 LTVSQVAAVATCHDR-RVTVELAGESRPGVKASSDWVIDSMSRGTDSYGVTTGFGATSHR 59
                                                                    TDHLTHKLKHHPGQIEAAAIMEYILDGSDYVKAAQKVHEMDPLQKPKQDRYALRTSPQWL
                                                                                                                                                                                                                                                                                                                                                                         AITKFLNNNITPCLPLRGTITASGDLVPLSYIAGLLTGRPNSKAVGPTGEVLNAEKAFAA 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EEFDRVFTAMC 688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EKDLLKVVDREYVYAYVDDPCSATYPLMQKLRQVLVDHAMMNGEKEKNSSTSIFQK1GAF 616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EKOLLEVVOREYVEAY IODVOSGTYPI.MQKI.RQVI.VOHAI.NNGETEKNTNTSIEGKIATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EAVDILKIMSSTYLVALCQAIDLRHLEENLKQTVKNTVSQVAKRVLTMGINGELHPSRFC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EAVDILKEMSSTYLVALOQSIDLEHLEENMKSTVKNIVSQVAKKVLIMSVNGELHESREC
TDHLTHKLKHHPG01EAAA1MEH1LDGSSY1KEAQKLHE1DPL0KPK0DRYALRTSPOWL
                                                                                                                                                    AEIDGGFFELQPKEGLALVNGTAVGSGLASIVLFEANLLVVLTEVLSAIFAEVMQGKPEF
                                                                                                                                                                                                                            AGVEGGEFELQPKEGLALVNGTAVGSGMASMVLFDANVLALLSEVLSATFAEVMOGKFEF 295
                                                                                                                                                                                                                                                                                                     AITKFLNHNITPCLPLRGTITASGDLVPLSYVAGLLIGRPNSKSIGPNGEDLNAKDAFKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                         RTKQGGALQNELIRELNAGIEGNGTEASHTLPYSSTEAAMLVRVNTLLQGYSGIREDIME 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          538;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EEFDKVFSAIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EEELKTLLPKEVESARTEYENGNPAISNKIKECRSYPLYKFVREELGCSLLTGEKIRSPG 676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Prkoullo6; Phe/His_NH3lyase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIGR01226; phe_am_lyase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           655 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71874 MW; 1F1DC76B49A538BF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77.4%; Score 2820.5; 82.0%; Pred. No. 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           655 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.5e-170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 10; Length 655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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DЪ	Qy	Db	Ϋ́	Dβ	Qy	Вb	Qy	Db	ŶΫ	DЬ	ŸΫ́
600	656	540	596	480	536	420	476	360	416	300	356
YKFVRESLGTSLQYGEKVKSPGEECDKVFTALCEGKFIDPMMDCLKKWNGSPLPIC 655	YRFVREELGRGFLTGEKVTSPGEEFDRVFTAMCKGQIIDPLLECLGGWNGEPLPIC 711	ALQNGEKEASSSTSIFHKIRAFEEELITLLPKEVENARVEVENGNSSIPNRIKECRSYPL 599	ALNNGETEKNTNTSIFQKIATFEEELKVLLPKEVEGVRIAYENDTLSIPNRIKACRSYPL 655	SQVAKRVLTTGINGELHPSRFCEKDLLKIVDHEYVFAYIDDPCSVTYPLMQKLRSVLVDH 539		QSAEQHNQDVNSLGLVSSRKTAEAEEILKLMSSTFLVALCQAIDLRHLEENMKNAVKNAV 479	QSAEQHNQDVNSLGLISARKTAEAVDILKLMSSTYLVALCQSIDLRHLEENMKSTVKNTV 535	KLMFAQFSELVNDFYNNGLPSNLTAGRNPSLDYGFKGAEIAMASYCSELQYLANPVTNHV 419	KLMFAQFSELVNDFYNNGLPSNLSGGRNPSLDYGFKGGEIAMASYCSELQFLANPVTNHV 475	GPQIEVIRHATKMIEREINSVNDNPLIDVSKNKALHGGNFQGTPIGVSMDNTRLAIASIG 359	356 GPĢTEVIRSSTKMIEKEINSVNDNPLIDVSRNKALHGGNPQGTPIGVSMDNTRLAIAAIG 415

Search completed: March 29, 2003, 02:12:14 Job time: 67 secs